į

```
; Search time 53.52 Seconds
(without alignments)
566.576 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
22. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
7. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
8. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
9. (SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
11. (SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
12. (SIDS1/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
13. (SIDS1/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
14. (SIDS1/gcgdata/hold-geneseqy-embl/AA1990.DAT:*
15. (SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
17. (SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
18. (SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
18. (SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
19. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
19. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
19. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
20. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
21. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
22. (SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-673-763-14
1333
1 MTPTLIVIPPSPPAPSYSA......QIRBTLSSPRKSASPSTKSS 273
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                     August 13, 2002, 09:23:46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_032802:
                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

14 :: 115 :: 15 ::

	Description		Amino acid comona	Amino acid souch	Chlematic acta sequenc	Chlamydia psicraci	Unman mitolin ric	Human mittorin and	Minotochock and in	Drosophila moleca	Donostic mite atil	Descrit Wile Bull	DOMESTIC MITE BILL
SUMMARIES	ID	AAY32176	AAY37087	AAY37086	AAY32173	AAY34783	AAR72826	AAW23996	AAR99795	ABB61012	AAE02245	AAEO2242	7
	DB	20	20	20	20	20	16	19	17	22	22	22	
a Query	Length	273	195	81	355	397	2482	2482	3248	1931	875	878)
% Query	Match	100.0	63.0	23.8	12.2	11.6	9.3	e.6	9.3	9.0	8.7	8.7	
	Score	1333	840	317	162.5	154.5	124.5	124.5	124.5	120	116	116	
Result	Q	Н	7	m	4	S	9	7	80	თ	10	11	

	Protein with Rho p	Male-enhanced anti	Mouse male enhance	human	_	=	9	Corn MFP1. Zea ma	cns		-	Human glial fibril	Partial protein en	1199	human	phila m		0.00	, Ē			Ø	02	60	_	human	t and o			kerat	tor fc	RHAMM 1-2a 1soform
AAE02246	AAW56473	AAW19540	AAW94391	ABG05280	ABG20258	ABB62816	AAB95460	AAB21233	Н	AAW56475	AAR51227	AAY20975	AAB21228	ABG20279	ABG08133	ABB70846	AAG50490	AAG50489	ABB61144	ABB61173	ABB62322	AAG26548	AAG26547	AAG26546	ABG05279	ABG20257	AAB58755	AAW23820	AAY 69289		AAR99673	AAR99675
22	13	18	20	22	22	22	22	21	22	19	15	19	21	22	22	22	21	21	22	22	22	21	21	21	22	22	21	18	21	21	17	17
1017	1372	1325	1325	881	881	622	789	672	1192	1388	334	433	398	2415	513	870	1081	1197	1690	1690	2013	430	458	473	176	777	433	469	469	546	909	631
8.7			•	•		٠															8.1							•	•	•	8.1	8.1
116	115.5	115	Ξ		113.5	12.	112	111.5	111.5	111.5	111	_	109.5	109	108.5	108.5	108.5	108.5	108.5	108.5	108.5	108	108	108	108	-	6	6	107.5	107.5	107.5	107.5
12	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	3.7	38	39	40	41	42	43	44	45

T 1 176 AAY32176 standard; Protein; 273 AA.	AAY32176;	01-FEB-2000 (first entry)	Chlamydia trachomatis infection-specific protein IncA.	IncA; infection; vaccine; therapy; diagnosis.	Chlamydia trachomatis.	WO9953948-A1.	28-OCT-1999.	20-APR-1999; 99WO-USO8744.		21-APR-1998; 98US-0082588. 22-MAY-1998; 98US-0086450.	(UYOR-) UNIV OREGON STATE.	Rockey DD, Bannantine JP;	WPI; 1999-633904/54. N-PSDB; AA234590.	Novel bacterial infection specific proteins for treating and diagnosing chlamydial infections
30L 732	AAY32	01-FE	Chlam	IncA;	Chlam	W0995	28-0C	20-AP	20-AP	21-AP	(UYOR	Rocke	WPI; N-PSDI	Novel chlamy
RES AAY XX	Y AC	DŢ	X CE	XX	SO	NA S	₹ 2 ×	PF	PR	PR PR	XX PA	I X	DR XX	T T X

```
W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1999
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY37086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                            ŏ
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                              SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESILDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                      IAPQITIVLLALFITSLAGNALYLQKTANLHLYODLQREVGSLKEINFMLSVLQKEFLHL 120
                 This sequence represents novel infection-specific protein IncA of Chlamydia trachomatis LGV-434 (serotype L2). IncA is found in the inclusion membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than with the refractile elementary body form. The invention includes: a
                                                                                                                                                                                                                                          1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                        Gaps
                                                                  vaccine directed against the reticulate body form of Chlamydia comprising 1 or more infection-specific proteins (see AAY32170-78), including IncA, IncB and InCC; methods of using and producing such a vaccine; methods for detection of infection-specific antibodies or antigens in a biological specimen; and a method of using therapeutic agents specifically directed against infection-specific chlamydial infection.
                                                                                                                                                                                                                                                                                                                                                                               SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                 100.0%; Score 1333; DB 20; Length 273; 100.0%; Pred. No. 2.6e-106; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                              241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                         A
 Page 45-46; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY37087 standard; Protein; 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0015041.
97FR-0016034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-IB01939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0107077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                      273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 - NOV - 1997
                                                                                                                                                                                                                         273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY37087;
   5;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                      ery Match
    Claim
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY37087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                       ŏλ
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                        ŏλ
                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                ò
   ò
```

```
ö
                                                                                                                                   AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, nonendemic trachoma, nongenococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, batholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 SLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIAL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 FATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKGSVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 840; DB 20;
91.5%; Pred. No. 3.2e-64;
iive 5; Mismatches 11
                                                                                             Disclosure; Page 892-893; 1755pp; English.
                                           Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY37086 standard; Protein; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0107077.
97FR-0015041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97FR-0016034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ynekragic 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 QRKESSDLC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1997;
17-DEC-1997;
```

8;

```
(GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9927105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffais R;
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34783;
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY34783
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
            δ
                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                   ó
                                                                                  AAY36754-127949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis. See AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and Thozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsable for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as perihepatitis, epidymitis, cervicitis, salpingitis, perihepatitis, barthollinitis; penemopathy in breast feeding infants; may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel bacterial infection specific proteins for treating and diagnosing
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents novel infection-specific protein IncA
                                                                                                                                                                                                                                            Length 81;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia psittaci infection-specific protein IncA.
                                                                                                                                                                                                                                        Score 317; DB 20;
Pred. No. 7.2e-20;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IncA; infection; vaccine; therapy; diagnosis.
                                     Genome sequence of Chlamydia trachomatis
                                                          Disclosure; Page 892; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           AAY32173 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 39-40; 56pp; English.
                                                                              AAY36754-Y37949 are encoded by
                                                                                                                                                                                                                                       23.8%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0082438.
98US-0082588.
98US-0086450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US08744
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2000 (first entry)
                                                                                                                                                                                                                                  Query Match
23.83
Best Local Similarity 98.53
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bannantine JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYOR-) UNIV OREGON STATE.
                   WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chlamydial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-633904/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia psittaci
                                                                                                                                                                                                        81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ34587
                                                                                                                                                                                                                                                                                                                                    |||||
76 iapqi 80
                                                                                                                                                                                                                                                                                                                       61 IAPQI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9953948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockey DD,
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                AAY32173;
                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAY32173
ID AAY3
XX
AAC AAY3
XX
DT 01-F
DE Chlai
XX
XX
XX
XX
XX
OS Chla
g
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                     ò
```

ō

```
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                               ----EV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                         154 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSLKEINFMLS--VLQKEFLH----LSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia psittaci strain GPIC. IncA is found in the inclusion membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than with the refractile elementary body form. The invention includes: a vaccine directed against the reticulate body form of Chlamydia comprising or more infection-specific proteins (see AAY32170-78), including or more infection specific proteins (see AAY32170-78), including nethods for detection of infection-specific antipodies or antigens in a biological specimen; and a method of using therapeutic agents specifically directed against infection-specific peptides, or the genes that code for such peptides, to treat chlamydial infection.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                            8 VIPPSPPAPSYSANRV-----PQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVG 58
                                                                                                                                                                                                                                                                                                                                                                   214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRKSAS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                59 FLIAPQITIVLLALFITSLA-----GNALYLQKTANLHLYQDLQR-----
                                                                                                                                                                                                                                                                        12.2%; Score 162.5; DB 20; Length
21.4%; Pred. No. 9.3e-06;
.ive 61; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY34783 standard; Protein; 397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                            63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30.
                                                                                                                                                                                                                      355 AA;
```

93US-0141239

```
22-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW23996;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                Lee W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
 12;
                     AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, shnusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584.Y35879) can be used inmunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                   124 itttletevkdikaakdqltleieafrnengnlkttaedleeqvsklseqlealerinql 183
                                                                                                                                                                                                                                                                                                                                                                                                            ----GFES-LLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEI 189
                                                                                                                                                                                                                                                                                                            60 LIAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLH 119
                                                                                                                                                                                                                                                                              Cell cycle; M phase; mitosin; retinoblastome; mitosis; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 RFL-----TPLAEEVRRLAHNQESLTAAIEELKTIRD-----SLRDEIGQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ALQR-----KESSDLCSQIRETLSSPRKSASPST
                                                                                                                                                                                                                                                             3 TPTLIVIP-PSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGF--
                                                                                                                                                                                                                                                                                                                             103;
                                                                                                                                                                                                              Length 397;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                  11.6%; Score 154.5; DB 20; 20.8%; Pred. No. 5.2e-05; ive 59; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                 LSKEFATTSKDLSAVSQDFYSCLQGFRD---NYK-----
     Page 760-761; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1480..1659
/label= internal_repeat
1660..1839
/label= internal_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR72826 standard; Protein; 2482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US12162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                est Local Similarity 20.8 atches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 QLSKTLTSQI-----
                                                                                                                                                                                 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mitosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-0CT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9511309-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR72826;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                     151
```

gg

g οy

g δ

οy g δ Ω õ

g

ò

```
AAR ARR72829 is human mitosin. Mitosin is involved in the regulation of the mammalian mitotic cell cycle. Mitosin as with E2F-1 (see AAR72824) conteracts with the retinoblastoma protein (the retinoblastoma tumour interacts with the retinoblastoma protein (the retinoblastoma tumour conteracts with the retinoblastoma tumour conteracts with the retinoblastoma tumour contents, is chosely associated with the centromeres/Kinetochores at the mitosic, is closely associated with the centromeres/Kinetochores at the mitotic spindle poles. Mitosin is necessary for a cell to mitotic cell to mitotic cell to conter the M phase of the mitotic cell cycle and its degradation is necessary for a cell to advance on to the next stage. Mitosin is thus contenting the M phase.

Consecul for controlling cell growth as overexpression of mitosin prevents a call from exiting the M phase.

Consecul for mitosin antibody, antibody fragment or a phosphorylated mitosin antien (or nucleic acid encoding it) can also be used to inhibit cell division which is particularly useful for the study of the cell cycle.

A further use is to control hyperproliferative cells, and so control alseases such as psoriasis and breast cancer. It can also be used to control control myperproproliferative cells, and so control control myperproliferative cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAGNALYLQK----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purified mammalian protein mitosin and agents that bind it and inhibit its action - used to promote cell growth or to inhibit cell division and/or proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitosin; phosphoprotein; mitotic cell cycle; antibody; analogue; inhibition; M phase; Antagonist; hyperproliferative cell; cancer; leukaemia; lymphoma; chromosome segregation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 2482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 124.5; Di
Pred. No. 0.23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nnskseagglkqeimtlkeeqnkmqkevndllqe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mitosin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW23996 standard; Protein; 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Scc
26.2%; Pre-
tive 32;
                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 8B; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 26.2
Matches 56; Conservative
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                WPI; 1995-170229/22.
N-PSDB; AAQ86851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                          Zhu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1998
```

ж Э

```
New isolated mitosin protein and gene - useful for, e.g. developing products for therapy and diagnosis of hyper-proliferative disorders
                                                                                                  /label= "Bipartite targeting motif"
/note= "Optionally C or G"
                                                                                                                                          /label= "Bipartite targeting motif"
/note= "optinally A or T"
                 'note= "leucine heptad repaet"
                                                                         'note= "leucine heptad repeat"
                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 40-52; 43pp; English.
  ocation/Qualiflers
                                                                                                                                                                                                                                                                                                                     such as cancers or psortasis
                                                                                                                                                                                                                   94US-0328254.
93US-0141239.
                        340..362
544..593
1387..1443
1885..1962
                                                                                                                                                                                                    94US-0328254
                                                                   ..2187
                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
          58..280
                                                                                                                                                                                                                                                                           WPI; 1998-109817/10.
N-PSDB; AAV09076.
                                                                                                                Misc-difference
Misc-difference
Misc-difference
                                                                                 Misc-difference
                                                                                        Misc-difference
                                                                                                                                                                                                                                                            Zhu X;
                                                                                                                                                                                                  24-OCT-1994;
                                                                                                                                                                                                                           22-OCT-1993;
                                                                                                                                                                                                                   24-OCT-1994;
                                                                                                                                                                  JS5710022-A.
                                                                                                                                                                                   20-JAN-1998
 Key
Domain
                                         Domain
Domain
                         Domain
                                  Domain
                                                         Domain
                                                                 Domain
                                                                                                                                                                                                                                                            Lee W,
```

This is the amino acid sequence for mitosin, a phosphoprotein necessary for the cell to ente mitosis. The protein's degradation is also necessary for the cell to advance into the next stages of mitosis. The mitosin protein, can be used to control the growth of cells. An can inhibit the mitotic cell cycle by preventing the cells from entering can inhibit the mitotic cell cycle by preventing the cells from entering can inhibit the mitosin of mitosin or its functional equivalent, would inhibit the cycle by preventing cells from entering equivalent, would inhibit the cycle by preventing cells from leaving the M phase. Antagonists to this protein can be used to control hyperproliferative cells in, (e.g. thyroid hyperplasis, Grave's disease, cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, cancer and various leukaemias and lymphomas). Reintroduction or control concleto and other neoplasms, bladder cancer, colon cancer, colon cancer, canced encoding the protein into a cell can restore defective chromosome segregation, which is a marker of progressing malignancy.

Can also be used for the detection and diagnosis of hyperproliferative

2482 AA; Sequence

88888888888888

.. 6 77 LAGNALYLOK-----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126 43; Query Match 9.3%; Score 124.5; DB 19; Length Best Local Similarity 26.2%; Pred. No. 0.23; Matches 56; Conservative 32; Mismatches 83; Indels ò g

DB 19; Length 2482;

```
374 ereksiselsdgykgeklillgrceetgnayedlsgkykaageknsklecllnectslce 433
                                                             -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding kinetochore protein – used as a marker for the G2 and Pphases of a cell cycle, partic. for detection of malignant diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A 372 kDa human kinetochore protein, CENP-F (AAR99795), is detected by immunofluorescence microscopy only during the G2 and M phases of a cell cycle. It is the product of a cDNA clone (AAT34578) isolated from a breast carchioma cDNA library. Recombinant CENP-F can be produced by expression in prokaryotic or eukaryotic host
                                           177 DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç
                                                                                                                                                                                                                                                                                                                                                                                                       1380..1610
/label- Globular_domain
/note- "globular domain consists of 2 direct
                                                                                                                                                                                                                                                                                  protein; CENP-F; cell cycle; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /laber-
3048.3248
3048.3248
7.abel- C-terminal domain is predicted
/note- "the C-terminal domain is predicted
form a proline-rich (10.6%) highly
basic (pI 10) globular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                             repeats of 95 amino acids"
                                                                                                                                                                                                                                                                                                                                                                   label Extended_coiled_structure
                                                                                                                                                                                                                                                                                                                                                                                              label Extended_coiled_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label = Extended_coiled_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1850. 2990
/label- Extended_coiled_structure
                                                                                                             228 -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 41-54; 72pp; English.
                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FOXC-) FOX CHASE CANCER CENT.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                 AAR99795 standard; Protein; 3248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US16216,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0353700.
                                                                                                                                                                                                                                                          Kinetochore protein CENP-F.
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yen TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-287116/29.
N-PSDB; AAT34578.
                                                                                                                                                                                                                                                                                              autoimmune antibody
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9617867-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1994;
                                                                                                                                                                                                                                                                                 Kinetochore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattner JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-1996.
                                                                                                                                                                                                         AAR99795;
                                                                                                                                                                                                                                                                                                                                               Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
Domain
127
                                                                                                                                                                      AAR99795
                                                                                                                                                                                 d
                                                                   Db
                                                                                              ò
ò
                                           ò
```

```
(ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chua KY,
                                                                                                                                                                                                                                                                                                                                                                    AAE02245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhinitis
                                                       Sequence
                                                                                      Query Match
Best Local $
                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                             146
                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                    248
                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                       AAE02245
                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                      g
                                                                                                                                                                                                 g
                                                                                                                                                                                                                        ά
                                                                                                                                                                                                                                             Dp
                                                                                                                                                                                                                                                                     δλ
 SSSSX
                                                                                                                                   ò
                                                                                                                                                                             ò
                                                                                                             .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176 ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                      1006 ereksiselsdgykgeklillgrceetgnayedlsgkykaageknsklecllnectslce 1065
                                                                                                                                                  LAGNALYLQK-----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                                                                                                                                                                                                                          227
                                                                                                               Gaps
                                                                                                                                                                                127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL----FSQEIIA
                                                                                                                                                                                                                          177 DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
 cells. CENP-F can be used to detect autoimmune antibodies to the protein, which may provide an early diagnosis for the onset of various malignant diseases. Use of CENP-F as a cell cycle marker allows the specific detection of G2 and M phase cells.
                                                                                       Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9828; 21pp + Sequence Listing; English.
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 9828.
                                                                                         DB 17;
                                                                                                               83;
                                                                                        Score 124.5; Di
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                            nnskseagglkgeimtlkeegnkmgkevndllge 1152
                                                                                                                                                                                                                                                                       -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers
                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                   ABB61012 standard; Protein; 1931
                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWD,
                                                                                            9.3%;
26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
N-PSDB; ABL05115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                            3248 AA;
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                          ABB61012;
                                                                                             Query Match
Best Local 8
                                                             Sequence
                                                                                                                                       11
                                                                                                                                                                                                                                                                        228
                                                                                                                                                                                                                                                   1066
                                                                                                                                                                                                                                                                                               1119
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                          ABB61012
```

:

q

g ò

õ

염

ò

ò

55555×8

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to immunogenic proteins, referred to as Bt allergens, derived from domestic mite (Blomia tropicalis). The specific Bt allergens of the invention includes Bt11, Bt10, Bt5 and BtA2. The
                            from WIPO
                                                                                                                                                                                                                                                                                                                     1413 lhaydklvceyerlkgclsdsnklsenlqkkverlhaeqlalqegisgrdselkqlrsel 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 LHLYQDL----QREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel immunogenic protein derived from house mite, Blomia tropicalis useful for treating and diagnosing conditions involving induction of immuneresponse to mite, such as allergic asthma, atopic dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mite; immunogenic protein; Bt allergen; therapy; atopic dermatitis; immediate hypersensitivity; systemic anaphylaxis; allergic rhinitis; asthma; antiallergic; antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                            Gaps
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R-FLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKE-
                                                                                                                                                                                                                                                                                                                                                                         --GFESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLR-----EEI
                                                                                                                                                                                                                          32;
                                                                                                                                                                           Length 1931;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                            89;
                                                                                                                                                                        Score 120; DB 22;
Pred. No. 0.4;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 162-166; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE02245 standard; Protein; 875 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1592 drrskelgevtkdcenirsdlea 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SSDL-----CSQIRETLSS 261
                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99SG-0005313.
2000AU-0008842.
2000AU-0008844.
2000AU-0008845.
                                                                                                                                                                                   9.0%;
24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domestic mite Btll allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2000; 2000WO-AU01227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYSI-) UNIV SINGAPORE NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheong N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-308609/32
                                                                                                                                                                                                        Local Similarity
nes 49; Conserv
                                                                                                          1931 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blomia tropicalis
                                                                                                                                                                                                                                                                                                                                                                                   RDNYK - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD06237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200130817-A1
```

```
'n,
immunogenic protein is useful for preventing, reducing or ameliorating immediate hypersensitivity condition such as atopic dermatitis, immediate hypersensitivity, systemic anaphylaxis, allergic rhinitis or asthma and for modulating an immune response directed to Bt allergen in directed to all or a part of Bt allergen in a biological sample from a subject. The Bt allergens are also useful for detecting antibody subject. Antibodies to Bt allergen in a biological sample from subject. Antibodies to Bt allergens are also used as therapeutic or diagnostic agents, to screen Bt immunoassays and as antagonists to inhibit Bt activity under circumstances where temporary hypersensitivity inhibition is required. The present sequence is Btll allergen.
                                                                                                                                                                                                                                                                           94 QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                 154 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mite; immunogenic protein; Bt allergen; therapy; atopic dermatitis; immediate hypersensitivity; systemic anaphylaxis; allergic rhinitis; asthma; antiallergic; antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to immunogenic proteins, referred as Bt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel immunogenic protein derived from house mite, Blomia tropicalis useful for treating and diagnosing conditions involving induction of immuneresponse to mite, such as allergic asthma, atopic dermatitis,
                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                  214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRK 264
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                          0.3;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                     8.7%; Score 116;
llarity 26.9%; Pred. No. 0
Conservative 31; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE02242 standard; Protein; 878 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domestic mite Btll allergen #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 3; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2000; 2000WO-AU01227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-1999; 99SG-0005313.
18-JUL-2000; 2000AU-0008842.
18-JUL-2000; 2000AU-0008844.
18-JUL-2000; 2000AU-0008845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYSI-) UNIV SINGAPORE NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheong N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-308609/32.
                                                                                                                                                                         875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blomia tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD06236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200130817-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2001
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE02242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chua KY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8$$88888888888
                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                               쉽
```

```
ŝ
allergen, is derived from domestic mite, Blomia tropicalis. The specific limmunogenic protein is useful for preventing, reducing or ameliorating blomia tropicalis hypersensitivity condition such as atopic dermatitis, immediate hypersensitivity, condition such as atopic dermatitis, asthma and for modilating an immune response directed to Bt allergen in a subject. The Bt allergens are also useful for detecting antibody clirected to all or a part of Bt allergen in a blological sample from a subject. Antibodies to Bt allergens are also used as therapeutic or diagnostic agents, to screen Bt immunoassays and as antagonists to inhibit Bt activity under circumstances where temporary hypersensitivity inhibition is required. The present sequence is Btll allergen.
                                                                                                                                                                                                                                              QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                              154 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mite; immunogenic protein; Bt allergen; therapy; atopic dermatitis; immediate hypersensitivity; systemic anaphylaxis; allergic rhinitis; asthma; antiallergic; antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                             214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRK 264
                                                                                                                                                                                                                                                                                                                                                             Length 878;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                           72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domestic mite Btll allergen polymorphic variant.
                                                                                                                                                                                                     ; DB 2
                                                                                                                                                                                                  8.7%; Score 116; DB
26.9%; Pred. No. 0.31
:ive 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Encoded by TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                AAE02246 standard; Protein; 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note- "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Encoded
                                                                                                                                                                                              Query Match
Best Local Similarity 26.98
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                               878 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blomia tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200130817-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-2001
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE02246;
                                                                                                                                                                                                                                                 94
   8$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
The present invention relates to immunogenic proteins, referred as Bt allergen, is derived from domestic mite, Blomia tropicalis. The specific bt allergens of the invention includes Btl1, Btl0, Bt5 and BtA2. The immunogenic protein is useful for preventing, reducing or ameliorating immunogenic protein is useful for preventing, reducing or ameliorating immunogenic protein is useful for preventing, reducing or ameliorating an immune response directed to Bt allergen in asthma and for modulating an immune response directed to Bt allergen in a subject. The Bt allergens are also useful for detecting antibody directed to all or a part of Bt allergen in a biological sample from a cubject. Antibodies to Bt allergens are also used as therapeutic or diagnostic agents, to screen Bt immunoassays and as antagonists to inhibit Bt activity under circumstances where temporary hypersensitivity inhibition is required. The present sequence is a protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                        Novel immunogenic protein derived from house mite, Blomia tropicalis useful for treating and diagnosing conditions involving induction of immuneresponse to mite, such as allergic asthma, atopic dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative P. abyssi ATPase involved in DNA repair #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 116; 26.9%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB96721 standard; Protein; 1177 AA.
                                                                                                                                                                                                                                                                                      Claim 6; Fig 7; 230pp; English.
                                           2000AU-0008842.
2000AU-0008844.
2000AU-0008845.
                                                                                                                                      Lee BW;
                              99SG-0005313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
10-OCT-2000; 2000WO-AU01227
                                                                                                      (UYSI-) UNIV SINGAPORE NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                     Chua KY, Cheong N,
                                                                                                                                                                 WPI; 2001-308609/32.
N-PSDB; AAD06245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus abyssi.
                                           18-JUL-2000;
18-JUL-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB96721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

5

```
ŝ
                                                                                                                                                                                                                                                     The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rho protein-binding activity; protein kinase activity; inhibitor; smooth muscle fibre formation; smooth muscle contraction; circulatory disease; treatment; tumour formation; metastasis inhibitor; autoinmune disease; platelet aggregation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 726 eriikse-----iedsqkgieeidriihekkgeiaklrgkierlerkrdklkkalenp 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 lklrkea-----leaeinslkvelrglenggfelrikmseiekeitlltrdlekllse 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---EINFMLSVLQKEFLHLSKEFATTSKD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           earevtekirevegeigklreelsrvesrleslnsrlneeliprkasleeeieglvnkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RLAHNQE----SLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LDEYKNSTEEMRKLFSQ-
                                                                                                                                                                                 nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1177;
                                                                                                           ö
                                                                                                           Lecompte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein with Rho protein-combining and kinase activity.
                                                                                                                         <u>بر</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116; DB 22;
Pred. No. 0.45;
2; Mismatches 72;
                                                                                                          Thierry JC, Prieur D, Dietrich J,
Weissenbach J, Saurin W, Heilig F
                                                                                                                                                                                                                               Claim 7; Pages 1483-1487; 1657pp; French.
                                                                (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW56473 standard; Protein; 1372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 LSAVSQDFYSCLQGFRDNYKGFESL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 LYLQKTANLHLYQDLQREVGSLK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EIIADLKGSVASLREEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.78;
         99FR-0005034.
                                                                                                                                                                                                     proteins useful in industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                           WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                1177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 QIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-1998
                                                                                                                Forterre P,
Querellou J,
           21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         899 rmde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW56473;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW56473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
ŏ
```

sp

```
The present sequence represents a protein that has Rho protein-binding activity and protein kinase activity. Inhibitors of the Rho-binding protein kinase can be used to inhibit smooth muscle fibre formation and smooth muscle contraction. Other applications of the Rho protein-binding agent and its' products are as a circulatory disease treating agent, a tumour formation or metastasis inhibitor, an autolmmune disease treating agent or a platelet aggregation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOKTANLHLYQDLQREVGSLK-EINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IIADLKGSV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ASLREEIRFLTPLAEEVRRLA--------HNQESLTAAIEELKTIRDSLRDEIG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               773 qkinellkgkdvlnedvrnltlkiegetgkrcltgndlkmgtgqvntlkmsekglkgenn 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           667 lekrglgerftdlekeknnmeldmtyglkviggslegeetehkatkarla------
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 1372;
                                                                                                                                                                                                                                 ۲
                                                                                                                                                                                                                        Bovine and human Rho protein-binding protein kinase - used develop products for treatment of smooth muscle disorders, circulatory disease, cancer and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key Location/Qualiflers
Misc-difference 305..320
/note= "Not shown in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8.7%; Score 115.5; DF ilarity 21.5%; Pred. No. 0.61; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 QGFRDNYKGFESLLDEYKNSTEEMRKLFSQE-----
                                                                                                                                                                                                                                                                         Disclosure; Pages 35-39; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 QLSQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW19540 standard; Protein; 1325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; MEA-2; detecting mutation.
                                                                                                      95JP-0325129.
96JP-0017150.
96JP-0131206.
                                                                 96JP-0324594
                                                                                          96JP-0241061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                          (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Male-enhanced antigen-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus domesticus.
                                                                                                                                                                                  WPI; 1998-315475/28.
                                                                                                                                                                                                                                                                                                                                                                                                            1372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                 N-PSDB; AAV23127
            JP10113187-A
                                                                                                      20-NOV-1995;
05-JAN-1996;
26-APR-1996;
                                                               20-NOV-1996;
                                      06-MAY-1998.
                                                                                         23-AUG-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S.
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW19540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW19540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
2222222222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

4

```
The present sequence represents male-enhanced antigen-2 (MEA-2), which has been derived from a domestic mouse. The polynucleotide encoding the protein can be used for the detection of mutations affecting the MEA-2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 SKDLSAVSQDFYS---CLQGFRDNYKGFESLLDEYKNSTE----EMRKLFSQEII---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                68 VLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 kktvevehsrlqkdmslvhqqmaeleghlqsvqke---rdemeihlqslkfdkeqmialt 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                   Male-enhanced antigen Mea-2 gene - especially from mouse, useful for
                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                              Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|:: :|: | : | :| | :| | :| | | :| | | :| | | :| | | :| | eanetlkkqi-eelqq--eakkaiteqkqkmkrlgsdltsaqke 825
                                                                                                                                                                                                                                                                                                                                                                             Score 115; DB 18;
Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                        ch 8.6%; Score 115; DB Similarity 21.4%; Pred. No. 0.65 48; Conservative 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 13, 2002, 09:23:49
Job time: 150 sec
                                                                                                                                                                                                                              Claim 8; Page 9-10; 13pp; Japanese.
                                                        95JP-0311638
                                                                                   95JP-0311638
                                                                                                                                                                                                    detecting mutation(s)
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                        WPI; 1997-314229/29
                                                                                                                (ITOH-) ITO HAM KK.
                                                                                                                                                                                                                                                                                                                               1325 AA;
                                                                                                                                                         N-PSDB; AAT74034
JP09121869-A.
                                                                                  07-NOV-1995;
                                                      07-NOV-1995;
                            13-MAY-1997.
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

<u>.;</u>

us-09-673-763-14.rag

```
776
776
775
775
775
783
11147
11147
3289
3289
338
337
337
337
337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
ŏ
                                                                                                                         August 13, 2002, 09:24:18; Search time 23.55 Seconds (without alignments) 283.150 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16, Appl
1, Appl
15, Appl
4, Appl
1, Appl
1, Appl
3, Appl
3, Appli
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 11, Apsequence 15, A sequence 1, Apsequence 1, Apsequence 1, Apsequence 12, A sequence 12, A sequence 12, A sequence 1, Apsequence 1, Apsequence 1, Apsequence 17, A sequence 11, A sequence 11,
                                                                                                                                                                                                                                                         1 MITPILIVIPPSPPAPSYSA.....QIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/fB_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-685-576-4
US-09-067-351-1
US-09-067-351-1
US-08-040-217A-3
US-08-700-178-3
US-08-995-654-3
US-08-688-576B-12
US-08-468-577B-12
US-08-468-577B-12
US-08-468-577B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-16216-1
US-07-603-133B-16
US-08-685-576-1
US-07-603-133B-15
                                                                                                                                                                                                                                                                                                                                                                                                       Otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-468-577B-17
US-08-089-397A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-470-950-4
US-08-467-781-4
US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-483-924-4
US-09-452-294-1
PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                  US-09-673-763-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2482
3248
3248
775
1388
1388
1388
546
546
477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477
604
604
604
604
22101
22101
22101
22101
2101
2101
712
712
712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124.5
124.5
124.5
111.7
111.5.5
111.5.5
111.5.5
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
100.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103.5
103.5
103.5
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
9, Appil
5, Appil
5, Appil
2, Appil
198, Appil
198, Appil
3, Appil
3, Appil
3, Appil
3, Appil
16, Appil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 LAGNALYLOK-----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhu, Xueliang
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
GORRESPONDRNCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Sequence 17
Sequence 18
Sequence 18
Sequence 18
Sequence 19
Sequence 5,
Sequence 5,
Sequence 5,
Sequence 5,
Sequence 3,
Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPOTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,254

FILING DATE: 24-OCT-1994

CLASSIFICATION: A35

PRIOR APPLICATION NUMBER: US 08/141,239

FILING DATE: 22-OCT-1993

ATTORNEY/AGENT INFORMATION:

RESTSTATION NUMBER: 31.815

REFERENCE/DOCKET NUMBER: 9-CJ 1191

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR EQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.3%; Score 124.5; DB 1;
Best Local Similarity 26.2%; Pred. No. 0.023;
Matches 56; Conservative 32; Mismatches 83;
                                                             US-08-089-397A-15
US-07-603-133B-14
US-07-603-133B-14
US-09-088-199B-9
5210183-3
US-08-477-260-5
US-08-471-491-5
US-08-471-491-5
US-09-227-357-198
US-08-451-2
US-08-451-2
US-09-317-223-3
US-09-659-849A-3
US-09-213-632-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-12675-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-726-214-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2482 amino acids
```

a

q

δ

g δ

ŏ

```
1006 EREKSISELSDOYKQEKLILLORCEETGNAYEDLSOKYKAAQEKNSKLECLLNECTSLCE 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI---- 227
                                                                                                                                                                                                                                                         APPLICANT: Trunchy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 LAGNALYLQK----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                        1066 NRKNELEQLKEAFAKEHQEFLTKLAFAEER---NONLML----ELETVQOALRSEMTDNQ 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3248;
    DLKGSVASLREEI - - - - RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US95/16216 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124.5; DB 5;
Pred. No. 0.034;
2; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dann Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                   1119 NNSKSEAGGLKQEIMTLKEEONKMQKEVNDLLOE 1152
                                                                                   --GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
RAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%; Scor.
26.2%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Phi
STATE: PA
COUNTRY:
                                                                                                                                                                                        RESULT 3
PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dβ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                  qq
                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1006 EREKSISELSDQYKQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNECTSLCE 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIA 176
                                    127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIA 176
                                                                                                                                       374 EREKSISELSDOYKQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNECTSLCE 433
314 LLSETLSLEKKEMSSIISLNKREIEELTQENGTLKEINASLNQEKMNLIQKSESFANYID 373
                                                                                                                 DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: THE METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NAMBER: US/08/353,700 FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%; Score 124.5; DB 1;
26.2%; Pred. No. 0.034;
utematches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                       487 NNSKSEAGGLKQEIMTLKEEGNKMQKEVNDLLOE 520
                                                                                                                                                                                                228 -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
TELECHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  equence 1, Application US/08353700
htent No. 5599919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 LAGNALYLQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-08-353-700-1
                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

ä

ò

ò

```
84 LQKTANLHLYQDLQREVGSLK-EINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                717 ----DKNKIYESIEERAKSEAMKEMEKKLSEERTLKQKVENLLLEARKRCSILDCDLKQSQ 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.7%; Score 115.5; DB 2; Length 1:
Best Local Similarity 21.5%; Pred. No. 0.065;
Matches 45; Conservative 34; Mismatches 81; Indels
                APPLICANT: Nakano, Takeshi
APPLICANT: ILO, Masaaki
APPLICANT: ILO, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                       143 QGFRDNYKGFESLLDEYKNSTEEMRKLFSQE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 QLSQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 HLLEMKMSLEKQNAELRKERQDADGQMKE 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-07-603-133B-15
; Sequence 15, Application US/07603133B
; Patent No. 5298244
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)...
TELEFAX: (204)...
TELEFAX: 904136
INFORMATION FOR SEQ.
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino acids
"YPE: amino acids
"YPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-685-576-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 QDLERQLGDLRE------FENSLSQEIAITQLIDLALLPLDMFSM-----FSGI 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 ESLLDEYKNSTEEMRKLFSQEITADLKGSVASLREEIRPLTPLAEEVRRLAHNQESL--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: 1jaz, Mohammed K.
APPLICANT: Jarker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
CORRESPONDENCE: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.8%; Score 117; DB 1; Length 775;
Dest Local Similarity 26.5%; Pred. No. 0.02;
Matches 40; Conservative 29; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER: IN EXPER ALLS
COMPOTER: IN FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Sulte 200
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9313-0004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 SEWTDVSEQIAGSSDSVRNISTQISAISRL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 ---TAAIEELKTIRDSLRDEIGQLSQLSKTL 237
                                                                                                     ; Sequence 16, Application US/07603133B
; Patent No. 5298244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: RODINS, RODETTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELERA: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEO ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH 775 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08685576
Patent No. 5906819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kalbuchi, Kozo
APPLICANT: Iwamatsu, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-1338-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                         USA
                                                                     RESULT 4
US-07-603-133B-16
                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                        94025
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-685-576-1
```

g à

```
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 SLKEINFMLSVLQKEFLHLSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGFESLLDEYK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 DLRE------FENSLSQEIAMTQLIDLALLPLDMFSM------FSGIKSTIDAAK 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 NSTEEMRKLFSQE----IIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEEL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 SMATKVMKKFKRSGLATSISELTGSLSNAASSISKSSSIRSNISSIS----VWTDVSEQI 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 LIGTIGFLALLGHLVGFLIAPQITIVLLALFITSLAGNALYLQKTAN-LHLYQDLQREVG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 KTIRDSLRDEIGQLSQLSKTLTSQIALQRKES---SDLCSQIRETLSSPRKSASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NOMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kaibuchi, Kozo
APPLICANT: Kaibuchi, Kozo
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Ito, Masaaki
APPLICANT: Tto, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-0CS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

8.5%; Score 113.5; DB 1;
Best Local Similarity 23.2%; Pred. No. 0.042;
Matches 55; Conservative 45; Mismatches 100;
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9313-0004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/603,133B FILING DATE: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/08685576
; Patent No. 5906819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNATION ROLLS TO STATE TO S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           775 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-603-133B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-685-576-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

```
----SQEIIADLKGSVASLR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 LQKTANLHLYQDLQREVGSLK-EINPMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 667 LEKROLQERFTDLEKEKSNMEIDMTYQLKVIQOSLEQEEAEHKATKARLADKNKIYESIE 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               727 EAKSEAMKEMEKKLIJEERTLKQKVENLLILEAEKRCSLLDCDLKQSQQKINELLKQKDVLN 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 EEIRFLT-PLAEEVRRLAHNGESLTAAIEELKTIRDS---LRDEIGQLSQLSKTLTSQIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1388;
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 111.5; DB 2; 22.1%; Pred. No. 0.15; tive 40; Mismatches 91;
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09067351
Patent No. 5994081
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Nell C.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: HUMAN KERATINS
                                                                                                                                                                                     24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 QGFRDNYKGFESLLDEYKNSTEEMRKLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16887/843
                                                                                                                                                                                                                                          FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION NUMBER: JP 8-17150
FILING DATE: 05-JAN-1996
FILING DATE: 05-JAN-1996
FILING DATE: 36-APR-1996
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1388 amino acids
                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 LQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     847 ELRKERODADGOMKE 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-685-576-4
                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                           Washington
                                                                 AY: USA
20007-5109
                           CITY: Washin STATE: D.C. COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-067-351-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
```

4;

```
326 ------MDNSRSLDLDGIIAEVKAQYEEMAKCSRAEABAWYQTKFETLQAQAGKHGDDL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 NALYLQKTANLHLYQDLQREVGSLK-EINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 YSCLQGFRDNYKG--FESLLDEYKNSTEEMRKLFSQEIIA--------DL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 KGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08402217A
Patent No. 5587301
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hawins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Scalhamer, Jeffrey J.
TITLE OF INVENTION: UMBLICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: INCTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SETVARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/360,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.1%; Score 107.5; DB 4; Best Local Similarity 24.1%; Pred. No. 0.091; Matches 48; Conservative 31; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
RECISTRATION UNDBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHRAPTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/067,351
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 LEAALQRAK-QDMARQLRE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 SQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 546 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter DI
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: PANCTUTO2
; CLONE: 1467090
US-09-360-490-1
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11ne
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-402-217A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 YSCLQGFRDNYKG--FESLLDEYKNSTEEMRKLFSQEIIA-------DL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 NALYLQKTANLHLYQDLQREVGSLK-EINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 -----MDNSRSLDLDGIIAEVKAQYEEMAKCSRAEAEAWYQTKFETLQAQAGKHGDDL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 KGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 546;
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COMPUTER: GALEFORN:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/067,351
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
8.1%; Score 107.5; DB 2;
Best Local Similarity 24.1%; Pred. No. 0.091;
Matches 48; Conservative 31; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NESOLI 5.
Sequence 1, Application US/09360490
Sequence 1, Application US/09360490
Settle 1, Sequence 1, Application US/09360490
Settle 1, Sequence 1, Application US/09360490
Settle 2, Sequence 1, Application Information In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNET/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELEFOMMUTGATION INFORMATION:
TELEFONS: (650) 845-055
TELEFAX: (650) 845-4166
INFORMATION FOR EAD ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||| : |: |:||
434 LEAALQRAK-QDMARQLRE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 SQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LIBRARY: PANCTUT02
| CLONE: 1467090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 PORTE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ζ,

```
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-995-654-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 TAQLESEQEKYNDTAQSLRDVTAQLESEQEKYNDTAQSLRDVTAQLESVQEKYNDTAQSL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 RDNYKGFESLLDEYKNST----EEMR--KLFSQEIIADLKGSVASLREEIRFLTPLAEEV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 RRLAHN-QESLTAAIEELKTIRDSLRDEIGQL-SQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 TANLHLYQDLQREVG-SLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hawkins, Phillip R.
APPLICANT: Wide, Craig G.
APPLICANT: Wide, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALINGOMAN RECEPTOR EXPRESSED IN HUMAN TITLE OF INVENTION: HYALINGOMAN RECEPTOR EXPRESSED IN HUMAN WHERE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.9%; Pred. No. 0.1;
Matches 43; Conservative 36; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/700,178
FILING DATE: August 20, 1996
CLASSIFICATION: 435
                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,217A FILING DATE: 10 MAR-1995
                                                                                                                      FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REGISTRATION NUMBER: 9F-0028US
REFERENCE/DOCKET NUMBER: PF-0028US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 3, Application US/08700178 atent No. 5783669 Patent No. 5783669 5700912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                     : 477 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: mouse
CLONE: GI 53979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-402-217A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
```

```
146 RDNYKGFESLLDEYKNST----EEMR--KLFSQEIIADLKGSVASLREEIRFLTPLAEEV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 TANLHLYQDLQREVG-SLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 RRLAHN-QESLTAAIEELKTIRDSLRDEIGQL-SQLSKTLTSQIALQRKESSDLCSQIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |----VSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQILTAESTNQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Wide, CIA 1

APPLICANT: Wide, CIA 1

APPLICANT: Sellhamer, Jeffrey

APPLICANT: Sellhamer, Jeffrey

TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN

TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows SOPTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: 4795,654 FILING DATE: December 22, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.9%; Pred. No. 0.1;
Matches 43; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5: Incyte Pharmaceuticals, Inc.
3174 Porter Dr.
                                                                                                                              PF-0028-1 DIV
                      US 08/402,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/700,178
APPLICATION NUMBER: 00, 1996
FILING DATE: August 20, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,
FILING DATE: MARCH 10, 1995
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: PF-00
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08995654 Patent No. 6025138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                             LENGTH: 477 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
LIBRARY: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 31/4 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: De CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                GI 53979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
```

7;

5

```
97 OREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 DEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEEL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                 Length 604;
                                                                                                                                                                                                                                                                                                                                                      Query Match
8.0%; Score 106; DB 2; Length 60,
Best Local Similarity 25.2%; Pred. No. 0.14;
Matches 38; Conservative 37; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08468579B
Patent No. 5981700
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
ZIP: 10591-3144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road CITY: Tarrytown STATE: New York
               FILING DATE: 17-FEB-1989
ATOREY/AGENT INFORMATION:
NAME: KULT G. BLISCOG
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.7-KGB
TELECOMMUNICATION INFORMATION:
TELEPRAX: (914) 332-1700
TELEFAX: (914) 332-1700
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARRCTERISTICS:
LEGGH: 664 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 KKLAASQIEKQRQOMDLARQQGEQIARQQQQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 KTIRDSLRDEIGQLSQLSKTLTSQIALQRKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,579B
FLING DATE: O6-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: O5-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: US 08-JUN-1992
RROR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: US 07/715,181
FILING DATE: US 07/441,703
PRIOR APPLICATION NUMBER: US 07/441,703
FILING DATE: US 0-DEC-1989
PRIOR APPLICATION NUMBER: US 07/441,703
FILING DATE: US 0-DEC-1989
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                            US-08-468-576B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-468-579B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                           87 TANLHLYQDLQREVG-SLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 RDNYKGFESLLDEYKNST----EEMR--KLFSQEIIADLKGSVASLREEIRFLTPLAEEV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 RRLAHN-QESLTAAIEELKTIRDSLRDEIGQL-SQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                         Query Match

8.0%; Score 106; DB 3; Length 477;
Best Local Similarity 23.9%; Pred. No. 0.1;
Matches 43; Conservative 36; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: System 7.5

SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,576B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08468576B
Patent No. 5955345
GENERAL INFORMATION:
APPLICATE RABIN, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
                                                                  PF-0028-2 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-UUN-1992
PRIOR APPLICATION NUMBER: US 07/715,181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/715,181 FILING DATE: 14-UN-1991 APPLICATION DATA: APPLICATION NUMBER: US 07/441,703 FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/312,543
                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-995-654-3
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abban
STREET: 6bu ...
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-468-576B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                        97 OREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEEL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ERRKGSLADV---VDTLKOKKL------EEMTRTEQEDSSCM------EKLL 157
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                       8.0%; Score 106; DB 2; Length 604; 25.2%; Pred. No. 0.14; .ive 37; Mismatches 48; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICANI.
TITLE OF INVENTION: DATAIN. DATAINED BY MOLECULAR CLONING NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESSE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road CITY. Tarrytown STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
                                                           REFERENCE/DOCKET NUMBER: MDI 251.5-KGB TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WOLDELIECL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,577B
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 06-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-UN-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 04-DEC-1989
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 17-FEB-1989
FILING DATE: 17-FEB-1989
FILING DATE: 17-FEB-1989
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 KTIRDSLRDEIGQLSQLSKTLTSQIALQRKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08468577B
Setent No. 6001804
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: System 7.5 SOFTWARE: WordPerfect
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 25.2%
Matches 38; Conservative
                                                                                                                                                                                                                            ; TYPE: amino acid; TOPOLOGY: linear US-08-468-579B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-468-577B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 QREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 DEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEEL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Gaps
                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 106; DB 3; Length 604; ilarity 25.2%; Pred. No. 0.14; Conservative 37; Mismatches 48; Indels 3
NAME: KULT G. BIISCOE
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.8-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPRAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
LENGTH: 604 amino acids
LENGTH: 604 amino acids
TERE: A mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 KTIRDSLRDEIGQLSQLSKTLTSQIALQRKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 13, 2002, 09:24:21 Job time: 152 sec
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                            US-08-468-577B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
```

٠.

		T.
,		
	`	
	,	
		•

ì

```
August 13, 2002, 09:24:53; Search time 29.79 Seconds (without alignments) 880.577 Million cell updates/sec
                                                                                                                                                               US-09-673-763-14
1333
1 MTPTLIVIPPSPPAPSYSA.....QIRBTLSSPRKSASPSTKSS 273
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

    protein search, using sw model

                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                   Scoring table:
                                                           OM protein
                                                                                              Run on:
```

tal number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

283138 seqs, 96089334 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	071R89	probable i	inclusion		hypothetical		intermediate	1380// hypothetical coile	probable		AJOJJY Giantin - human	outer laye			hypothetical	methyl-accepting c		G86517 hypothetical prote	probable memb	'8012/	hypothetical	outer layer p	chromosome s	2 intermediat	S70633	hungthat ton 1	4	mare-enginenced a	cardiac musc	oncer tayer protei
	DB		٠,	۰,	1 (٦ ٢	4 C	4 (4 C	٥, ١		٠,	4 ^	۰,	۹ (4 C	4 C					٦,	٦,	~	~	N	N	N			
	Length	273	276	3 10	000	000	472	100	1170	347	3250	777	3225	1286	700	0 ×	1 4 4 4	14/0	4 4	0 10	0 0	876	0//	//11	567	1388	1974	1325	1538	775	233
æ	ery	98.3	53.6	12.2	11.	11:	1 0	. 0	9 10	. 6	0	. 0	6	6	, 0		, α		. c		1 .		. 1				8.7	9.6	9.8	8.6	0
	Score	1311	714	162.5	154.5	154.5	128.5	128.5	126	124	122.5	122	121.5	120.5	120	120	117.5	116.5	116.5	116.5	110		116	115	116.5	110.5	115.5	_	•	11	112 5
	Result No.	-	7	æ	4	Ŋ	ø	7	ω	6	10	11	12	13	14	15	16	17	18	61		2.5		4 6	3 6	7 1	572	97	27	28	5

	2 C C C C C C C C C C C C C C C C C C C	7
unknown protein, 7 apolipoprotein A-1 hypothetical prote colled coil protein probable nuclear p dynein beta heavy outer layer protein probable vesicular probable vesicular probable vesicular probable vesicular probable victular probable vesicular probable vesicular probable vesicular fransport protein glial fibrillary a outer capsid prote hypothetical prote myosin-3 heavy cha	MENTS hlamydia trachomatis (serotype D, strain -Sep-1998 #text_change 08-Oct-1999 .: Fan, J.; Marathe, R.; Aravind, L.; Mit ntracellular pathogen of humans: Chlamydi	A.Residues: 1-273 - UNA A.Residues: 1-273 - UNA A.Cross-references: GB.AE001286; GB.AE001273; NID:93328516; PIDN:AAC67710.1; PID:933 A.Experimental source: serotype D, strain UW-3/Cx G.Genetics: A.Gene: incA
C96667 FPRTA4 FPRTA4 T738435 T741023 T750203 S62509 AD1313 AD30303 AB731 G72593 T38774	ALIGN protein A - C matis :revision 13 ; Lammel, C.J an obligate 1 MUID:99000809	GB:AE001 , strair
01000000000000000	rote Lis rev Lam	Θ . D
555 397 407 750 1837 775 1049 1104 11251 1251 1251 175 533	ALI embrane protein A - trachomatis #sequence_revision lman, S.; Lammel, C , 1998 ence of an obligate A71570; MUID:990008	s: DNA 173 <arn> ICES: GB:AE001286; GE SOURCE: SEROTYPE D,</arn>
ಹಹಪಡಪಡಪಡಪಡಪಡಪಡಪಡ ಬಹತತತತತತನನನನ್ನು ಪ್ರಪ್ತಣೆ	Lon mem nydia t 1998 #ss 1959 #ss 1559, 1-759, 1-759, 1-759, 1-759, 1-759, 1-759, 1-759,	JNA 3 <arn) es: GB</arn)
113.5 112 112 112 111.5 111.5 111.5 111.5 111.5 111.5 111.5 111.5 111.5 111.5 111.5	RESULT C71553 Probable inclusion membrane protein A C.Species: Chlamydia trachomatis C.Species: Chlamydia trachomatis C.Species: Chlamydia trachomatis C.Species: T3-Sep-1998 #sequence_revision C.Accession: C71553 R.Stephens, R.S.; Kalman, S.; Lammel, S.Science 282, 754-759, 1998 A.Title: Genome sequence of an obligat A:Reference number: A71570; MUID:99000 A.Stecssion: C71553 A.Stetus: preliminary	A) Residues: 1-273 cARNY A) Residues: 1-273 cARNY A) Cross-references: GB: A) Experimental source: C;Genetics: A,Gene: incA
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT C71553 C71553 C71563 C; Date: C; Date: C; Access R; Steph Science A; Title A; Title A; Cathus A; Access	A; Motecute Lype A; Residues: 1-2 A; Cross-referen A; Experimental C; Genetics: A; Gene: incA

ö 61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120 SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180 Gaps ö Indels Score 1311; DB 2; Pred. No. 4.6e-77; 1; Mismatches 4 241 IALORKESSDLCSQIRETLSSPRKSASPSTKSS 273 241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273 98.3%; 98.2%; Query Match
Best Local Similarity 98.29
Matches 268; Conservative 121 à g ογ q à g ò g ò qq

Length 273;

DB 2;

inclusion membrane localised protein IncA TC0396 [imported] - Chlamydia muridarum (stationation membrane localised protein IncA TC0396 [imported] - Chlamydia muridarum, Chlamydia trachomatis MoPn C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C; Accession: H81707 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke RESULT H81707

```
TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%;
ilarity 20.8%;
Conservative 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 QLSKTLTSQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B81560
A; Molecule type: DNA
A; Residues: 1-390 <REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Gene: CPn0186; CP0581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                      208
                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                   QQ
                       q
                                                        Qγ
                                                                                                                            A;Cross-references: GB:AE002306; GB:AE002160; NID:g7190428; PIDN:AAF39253.1; PID:g719043
A;Cross-references: GB:AE002306; GB:AE00E100; NID:g7190428; PIDN:AAF39253.1; PID:g719043
C;Genetics:
A;Gene: TC0396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psittaci gene coding for a protein
          Salzberg,
        , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255
A; Accession: H81707
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inclusion membrane protein A - Chlamydophila psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: |::||::|| SVISTPSLILMLAIMLVSEVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENLKAVNVELSEQINOLKOLHTRLSDFGDRLEANTGDFTALIADFOLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-355 <ROC>
A;Cross-references: EMBL:L35036; NID:9516598; PIDN:AAC41443.1; PID:9516599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                 113 LOKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                232
                                                                                                                                                                                                                                                                                                                                                              LGHLVGFLIAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                      1 MTTPTLIVIPPS--PPAPSYS-----ANRVPQPSLMDKIKKIAAIASLILIGTIGFLAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLIAPQITIVLLALFITSLA------GNALYLQKTANLHLYQDLQR------EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSLKEINFMLS--VLQKEFLH-----LSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIJADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSO
                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
                                                                                                                                                                                                                                    Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%; Score 162.5; DB 2;
llarity 21.4%; Pred. No. 0.0025;
Conservative 61; Mismatches 111;
                                                                                                                                                                                                                                  Score 714; DB 2; L
Pred. No. 8.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ockey, D.D.; Heinzen, R.A.; Hackstadt, T.
Microbiol. 15, 617-626, 1995
ptle: Cloning and characterization of a Chlamydia
eference number: $61491; MUID:95302975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASKTLSEQIASQIEENEKLYANITKALSQSYSDSS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSKTLTSQIALQRKESSDLCSQIRETLSSPRKSAS 267
                                                                                                                                                                                                                                                                        58; Mismatches
                                                                                                                                                                                                                                           53.6%;
52.7%;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 VIPPSPPAPSYSANRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-355 <ROC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
63; Conser
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S61491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S61491
                                                                                                                                                                                                                                                Query Match
Best Local Sim
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
Matches 63;
                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
```

```
hypothetical protein CP0581 [imported] - Chlamydophila pneumoniae (strains CWL029 and C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae, C; Species: Chlamydophila pneumoniae, C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C; Accession: A72108; B81560 C; Arcession: A72108 A; A72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002217; GB:AE002161; NID:97189493; PIDN:AAF38399.1; PID:9718
A;Experimental source: strain AR39, HL cells
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain J138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITTTETEVKDIKAAKDQLTLEIEAFRNENCNLKTTAEDLEEGVSKLSEQLEALERINQL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 IQANAGDAQEISSELKKLISGWDSKVVEQINTSIGALKVLLGQEWVQEAQTHVKAMQEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TPLAEEVRRLAHNQESLTAAIEELKTIRD-----SLRDEIGQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LIAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ALQR----KESSDLCSQIRETLSSPRKSASPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHETSLQQRIDAMLAQEQNLAEQVTALEKMKQEAQKAESEFIACVRDRIFGRRETPPPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ALTPGIGIALLVIFFVSMVLLGLILKDSISGGEBRRLREEVSRFTSENQRLTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GFES-LLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TPTLIVIP-PSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TPSAPNIPIPAPTTPGIPTTK-PRSSF---IEKVIIVAKYILFAIAATSGALGTILGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
                                                                                      EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRKSAS 267
                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154.5; DB pred. No. 0.0092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSKEFATTSKDLSAVSQDFYSCLQGFRD---NYK----
```

Ouchi, K.; Shiba, T.;

RGTNESLERQIHEMEDTHNAEVMGYQDTIGQLDNELRTTKSEMARHLREYQDL 373

```
C;Genetics:
A;Gene: SPDB:SPACIF3.06c
A;Map position: 1
             321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
             8
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intermediate filament - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: 541720
R:Glasgow, E.; Druger, R.K.; Fuchs, C.; Lane, W.S.; Schechter, N.
Tille: Molecular cloning of gefiltin (ON(1)): serial expression of two new neurofilame
Reference number: 541720; MUID:94147974
                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                           A Accession: B86514
A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-390 <STO>
A; Cross-references: GB:BA000008; NID:98978559; PIDN:BAA98396.1; GSPDB:GN00142
C; Genetics:
A; Gene: CPj0186
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
                                                                                                                                                                                                                                                                                                                 60 LIAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLH 119
                                                                                                                                                                                                                                                                                                                                     : | | | | | : | | : | | : | : | : | | | | : | | ALTPGIGIALLVIFFVSMVLLGLILKDSISGGEERRLREEVSRFTSENQRLTV----- 116
                                                                                                                                                                                                                                                                                                                                                                                                        177 IQANAGDAQEISSELKKLISGWDSKVVEQINTSIQALKVLLGQEWVQEAQTHVKAMQEQI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 QALQABILGMHNQSTALQKSVENLLVQDQALTRVVGELLESENKLSQACSALRQBIEKLA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 RFL------SLRDEIGQLS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 QLSKTLTSQI------ALQR------KESSDLCSQIRETLSSPRKSASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <GLA>
A;Residues: 1-472 <GLA>
A;Cross-references: EMBL:L19595; NID:g304478; PIDN:AAA88841.1; PID:g304479
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TPTLIVIP-PSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGF-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLQREVGS-LKEINFMLSVLQKEFLHLSK--EFATTSKDLSAVSQDFYSCLQGFRDNY-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KGFESLLDEYKNS----TEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                         ----GFES-LLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 QHETSLQQRIDAMLAQEQNLAEQVTALEKNKQEAQKAESEFIACVRDRTFGRRETPPPPTT
                                                                                                                                                                                                                            Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHNQESLTAAIEELKTIRDS----LRDEIGQLSQLSKTLTSQIALQRKESSDL 251
                                                                                                                                                                                               Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                         Score 154.5; DB 2;
Pred. No. 0.0092;
); Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>::</del>
<del>::</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 128.5; DB 2;
larity 28.9%; Pred. No. 0.54;.
Conservative 28; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                LSKEFATTSKDLSAVSQDFYSCLQGFRD---NYK-----
                                                                                                                                                                                11.6%; Scor.
20.8%; Pred
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                      Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Probable chromosome assembly protein - Pyrococcus horikoshil
C.Species: Pyrococcus horikoshil
C.Species: Pyrococcus horikoshil
C.Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C.Accession: F71190
R.Kawarabayasi, Y.; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamamoto, S.; Sawarabayasi, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogia, A.; Title: Complete sequence and gene organization of the genome of a hyper-thermophila A.Recession: F71190
A.Accession: F71190
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Mocolule type: DNA
A.Mocolule type: DNA
A.Residues: 1-1779
A.Residues: 1-1779
A.Residues: 1-1779
A.Residues: 1-1779
A.Residues: 1-1779
A.Residues: 1-1779
A.Residues: 1-1770
A.Resid
                                                                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
8
                                                                                                                                                             89 NLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDN 148
                                                                                                                                                                                                                           149 YKGFESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAH---N 205
                                                                                                                                                                                                                                                                                                                                                                                    QESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKTANLHLYQD-LQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQ 143
                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
             Length 1957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1179;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                            82;
             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 126; DB 2;
23.5%; Pred. No. 2.3;
tive 44; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: PH1798
C;Superfamily: chromosome segregation protein SMCI
                                                                                                Mismatches
    Score 128.5;
Pred. No. 3;
Query Match 9.6%; So
Best Local Similarity 27.1%; Pr
Matches 51; Conservative 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.5%,
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 ASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||:||
505 VSESTOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: thi
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
```

```
R;Gorziglia, M.; Green, K.; Nishikawa, K.; Taniguchi, K.; Jones, R.; Kapikian, A.Z.; J. Virol. 62, 2978-2984, 1988
A;Title: Sequence of the fourth gene of human rotaviruses recovered from asymptomatic A;Reference number: A28839; MUID:88275070
A;Accession: F28839
                C; Superfamily: rotavirus outer layer protein VP3
C; Keywords: capsid protein; coat protein; glycoprotein; hemagglutinin
E;1-240/Product: outer capsid protein VP8 #status predicted ...
F;241-246/Region: cleavage processing #status predicted
F;247-775/Product: outer capsid protein VP5 #status predicted
F;247-775/Product: outer capsid protein VP5 #status predicted ...
F;32,56,85,97,111,114,132,192,277,324,583,606/Binding site: carbohydrate (Asn) (coval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer layer protein VP3 - human rotavirus A (serotype 2 strain 1076)
N;Alternate names: hemagglutinin
N;Contains: outer capsid protein VP5; outer capsid protein VP8
C;Species: human rotavirus A
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 01-Mar-1996
C;Accession: F28839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | :|: |||
1584 EKLVKEIESLKSSKIAESTEWQEKHKELQKEYEILLQSYENVSNEAERIQHVVEAVRQEK 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 FITSLAGNALYLQKTAN-LHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSK-D 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLF-----SQEIIADLKGSVASLREEI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLS-QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 122; DB 1; Length 775; 26.8%; Pred. No. 2.5; tive 33; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3q13.31-3q13.31
C; Superfamily: giantin
C; Keywords: coiled coil; Golgi apparatus; transmembrane protein
F; 3238-3254/Domain: transmembrane #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 QDLQREVGSLKEINFMLSV-----LQKEFLHLSKEFATTSKDLSAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 SKTLTSQIALQRKESSDLCSQIRE--TLSSP-----RKSASPSTK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 23.6%; Score 122.5; Similarity 23.6%; Pred. No. 13; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Conservative
N; Alternate names: macrogolgin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: segment 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-775 <GOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 R---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternate names: protein BIK1 - yeast (Saccharomyces cerevisiae) (strain carlsbergensis) (Alternate names: protein YCL029c Alternate names: protein YCL029c Species: Saccharomyces cerevisiae Species: Saccharomyces cerevisiae Capecies: O6-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 06-Feb-1998 Capecies: O5-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 06-Feb-1998 Capecies: Of the EMBL Data Library, August 1994 Aspection: The polyfunctional HIS4 gene of Saccharomyces carlsbergensis: sequence Aspection: S5348 Aspection: S5348 Aspection: S5348 Aspection: The polyfunctional HIS4 gene of Saccharomyces carlsbergensis: sequence Aspectice: 1-347 CPOR> Aspection: The polyfunctional HIS4 gene of Saccharomyces carlsbergensis: sequence Aspectics: 1-347 CPOR> Aspection: The polyfunctional HIS4 gene of Saccharomyces carlsbergensis: sequence Aspectics: 1-347 CPOR> Aspective: The sequence of Saccharomyces Carlsbergensis: Sequence Aspectics: 1-347 CPOR> Aspectics: The sequence of Saccharomyces carlsbergensis: Sequence Aspectics: 1-347 CPOR> Aspectics: The sequence of Saccharomyces carlsbergensis: Sequence Aspectics: 1-347 CPOR> Aspectics: The sequence of Saccharomyces carlsbergensis: Sequence of Saccharomyces carlsbergensis: Sequence Aspectics: 1-347 CPOR> Aspectics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S70387; MUID:96363910
A;Reference number: S70387
A;Status; nucleic acid sequence not shown; translation not shown
A;Retus; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-347 <PQW>
A;Cross-references: BABL:013062; NID:9532779; PID:9532780
A;Cross-references: BABL:013062; NID:9532779; PID:9532780
A;Note: the source is designated as Saccharomyces carlsbergensis
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAEEVRRLAHNQ-----ESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 -ENEERNIAHNQPTDSSEDIELLKRQVEQLRSIEDQF-----ELHKTKWAKEREQLK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 KTANLHLYQDLQREVG-SLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 FRDNYKGF----ESLLDEYKNSTE-EMRKLFSQEIIAD-----LKGSVASLREEIRFLTP 194
                                                                                                                                                                                                                          724 -----KEEESLRSEIEDSERKIAEIDETISKKKDEVAKLKGRIERLEKRRDKLKKALEN 777
         668 EKVENLRIMKESLEGEVNSLR---VKLKALENQSFELRIRMSDVEKEISLISKDLEKLI-
                                                                                                                                                                                          ----REEIRFLTPLAEEVRRLAHNQESLTAAI-EELKTIRDSLRDEI-GQLSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 124; DB 2; Length 34<sup>o</sup>
27.1%; Pred. No. 0.72;
Live 25; Mismatches 86; Indels
                                                                      144 GFRDNYKGFESLLDEYKNSTEEMRKL----FSQEIIADLKGSVASL
                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                           : |:| : |:| | 838 NALKANINENEEALKSLTEKLEKLKKEEGEIYSRIEE
                                                                                                                                                                                                                                                                                                                    KTLTSQIALQRKESSDLCSQIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: SGD:BIK1
A;Cross-references: SGD:S0000534; MIPS:YCL029c
A:Map position: 3L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNDSLSKEYQNLSKELFSTKPQDSSS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 27.1
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
A56539
giantin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                           234 S--
                                                                                                                                                                                                    186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                   g
                                                                                                                                   q
                                                                                                                                                                                                                                                              pp
                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                ò
                                                                                                                                                                                                    οy
```

Ŋ

.; 6

Gaps

```
hypothetical protein alr4393 [imported] - Anabaena sp. (strain PCC 7120)
C; Species: Anabaena sp.
A; Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C; Accession: A12334
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabaeta A; Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterith A; Accession: A1234
A; Accession: A12354
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
G82490
methyl-accepting chemotaxis protein VCA0176 [imported] - Vibrio cholerae (strain N16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-496 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76092.1; PID:917133529; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4393
                                                                                                                                                                                                                       92 LYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSC---LQGFRDN 148
                                                                                                                                                                                                                                                                                 133 LOETIORAODDKKETETELESSRSRLHVLEKELSAKANDIFMYTKDLHDKNEELTSFRME 192
                                                                                                                                                                                                                                                                                                                                           149 Y------KGFESLLDEYKNSTEE------MRKLFSOEIIADLKGSVASLREE 188
                                                                                                                                                                                                                                                                                                                                                                                     189 IRFLTPL---ABEVRRLAHNQESLTAAIEE----LKTIRDSLRDEIGQLSQLSKTLTSQI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||: | ||:|| | | ||:|| || ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ANLHL------YQDLQREVGSLKEINFMLSVLQK------EFLHLSKEFATTSK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEII 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 DKKQVETQRDQAKKEKLKAQQDLAQTQAQYQRTQSRLGQVVTQYQKALAELQSVYNQR-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 ADLKGSVASLREEIRFLTPLAEEV----RRLAHNQESLTAAIEELKTIRDSLRDEIGQL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 IASLILIGTIGFLALLGHLVG------FLIAPQITIVLLALFITSLAGNALYLQKT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 496;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                       80;
                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                   y Match 9.0%; Score 120.5; D
Local Similarity 23.3%; Pred. No. 5.8;
hes 49; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 120; DB
21.9%; Pred. No. 2;
tive 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ALORKESSDLCSQIRETLSSPRKSASPSTK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 -MKNEELEDL----RQTTTASLGDSEQATK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQLSKTLTS---QIALORKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | | : : | | | | | : | SQLDKIIQNRNLEIA-QREE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLSAV-----
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: 152300
Solda, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ikehara, Y.
Sohda, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ikehara, Y.
Solda, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ikehara, Y.
Biochem. Biophys. Res. Commun. 205, 1399-1408, 1994
A;Title: Molecular Choning and sequence analysis of a human 372-kDA protein localized in A;Reference number: 152300; MUID:95100974
A;Reference number: 152300
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-325 CRES>
A;Cross-references: GB-D25542; NID:9662389; PIDN:BAA05025.1; PID:9808869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aubmitted to the EMBL Data Library, December 1995
A.Description: The sequence of C. elegans cosmid F59A6.
A.Reference number: 218526
A.Accession: T16507
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Gross-references: EMBL:041994; NID:g1123047; PID:g1123050; PIDN:AAAB3454.1; CESP:F59A6
A.Genetics: CESP:F59A6.5
A.Gene: CESP:F59A6.5
A.Gene: CESP:F59A6.5
A.Gross-references: EMBL:04094; NID:g1123047; PID:g1123050; PIDN:AAAB3454.1; CESP:F59A6
A.Gene: CESP:F59A6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glantin - human
N:Alternate names: gcp372
C;Species: Homo sapiens (man)
Species: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Aug-1999
469 FILLVPSNDDYQTPIMNSVTVRQDLERQLGDLRE------EFNSLSQEIAMTQLID 518
                                                                LSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIR 190
                                                                                                                                                                                                                           hypothetical protein F59A6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 QDLQREVGSLKEINFMLSV-----LQKEFLHLSKEFATTSKDLSAV-----S 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLF-----SQEIIADLKGSVASLREEI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FLTPLABEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLS-QL 233
                                                                                                          191 FLTPLAEEVRR---LAHNQESL---TAALEELKTIRDSLRDEIGQLSQLSKTL-TSQIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGNVSKQANLEATEKHDNQTNVTEEGTQSIPGETEEQDSLSMSTR 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 SKTLTSQIALQRKESSDLCSQIRE--TLSSP-----RKSASPSTK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 121.5;
; Pred. No. 15;
35; Mismatches
                                                                                                                                                                                                                                                                                                           244 QRKESS--DLCSQIRETLSSPRKSASPST 270
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.6%;
Matches 53; Conservative 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 R-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1730
   셤
                                                                õ
                                                                                                                       ద
                                                                                                                                                                              ò
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

Ξ

Gaps

```
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: G82490
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Auglure 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUD: 20406833
A; Accession: G82490
A; Status: preliminary
A; Messidues: 1.644 CHEI>
A; Residues: 1.644 CHEI>
A; Residues: 1.644 CHEI>
A; Cross-references: GB: AE004358; GB: AE003853; NID: 99657566; PIDN: AAF96089.1; GSPDB: GNO01
A; Genetics:
A; Genetics:
A; Gene: VCA0176
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSAVSQDFYSCLQGFR-----S 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|| :|| | | 467 LASTIQEIGSILDAIRGISEQTNLLALNAAIEAARAGDQCRGFAVVADEVRNLASRTASS 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 TEEMRKLFSQEIIADLKGSVASL------REEIRFLTPLAEEVRRLAHNQES 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 ITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSK---D 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 LTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toury Match 9.0%; Score 120; DB 2; Length 644 Best Local Similarity 19.2%; Pred. No. 2.7; Autches 44; Conservative 50; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 13, 2002, 09:24:56 Job time: 152 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                            simian 11 r
simian 11 r
mus musculu
mus musculu
caenorhabdi
human rotav
                                               homo sapien
rattus norv
                                                                                     human rotav
               sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=972;
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 YKGFESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAH---N 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 QESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSPRKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: | :: | || : | 450 RDFQNKKIRDFEKIEQDLRACLNSSSNELKERSALIDKRDGELNNLREQIKE----QKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                           Q16352
P23565
P39033
P12976
P17464
Q00547
P10567
P30214
P11196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1957;
                                                                                                                                                                                                                                                                                                                                 Tybe School Standard, Prr; 1957 AA.

2010411;
2010411;
31, Careted)
101-0CT-1996 (Rel. 34, Last sequence update)
101-0CT-1996 (Rel. 34, Last anotation update)
101-0CT-1996 (Rel. 34, Last anotation)
101-0CT-1996 (Rel. 34, Last sequence update)
101-0CT-1996 (Rel. 34, Last sequence upda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.6%; Score 128.5; F
27.1%; Pred. No. 1;
tive 32; Mismatches
                                                                                                                                                                                                                                                         ALIGNMENTS
                                                      AINX_RAT
VP4_ROTH3
VP4_ROTS1
VP4_ROTSS
VP4_ROTSS
SOX6_MOUSE
SOX6_MOUSE
MYSP_CAEEL
VP4_ROTH5
       CENE_HUMAN
APA1_MACFA
                                         AINX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z70690; CAA94624.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 51; Conserv
   000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 ASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 VSESTOSS 512
   7788888888888
 106.5
106
106
106
106
106
106
106
105.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                      урв6_scнро
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
CENF_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
 334
337
337
337
447
543
543
543
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                         % Search time 17.41 Seconds
(without alignments)
607.147 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human rotav
anabaena sp
human rotav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
homo sapien
bos taurus
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    porcine rot
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human rotav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human rotav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aquifex aeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human rotav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   schizosacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onchocerca
canine rota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  saccharomyc
gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methanococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feline rota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human rotav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                     ....QIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q06895
P08729
P17119
Q90988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9tu23
P46660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P40145
Q58718
P33741
Q07416
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 105224 seqs, 38719550 residues
                                                                                                                                                                                                          1 MTTPTLIVIPPSPPAPSYSA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFAP_HUMAN
MYS3_SCHPO
RA50_AQUAE
VP4_ROTHO
ALM1_SCHPO
OV71_OKVVO
VP4_ROTHO
TPR_HUMAN
KZC8_HUMAN

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        August 13, 2002, 09:30:42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YD86_SCHPO
VP4_RCTH1
Y7J3_ANASP
VP4_RCTHN
Y7J3_ANASP
VP4_RCTHN
VP4_RCTHN
YP4_RCTP
LAM0_DBROWE
LAM0_DBROWE
LAM0_DBROWE
VP4_RCTPH
VP4_RCTHN
YP73_SCHPO
USO1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTR1_HALN1
VP4_ROTF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2C7_HUMAN
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /P4_ROTHY
                                                                                                                                                                            US-09-673-763-14
1333
                                                                                                                                                                                                                                                                                                                                                                     Maximum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112.5
111.5
111.5
111.5
111.5
110.1
110.1
109.5
109.5
109.5
109.5
109.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
108.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112.5
                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

ŝ

Repeat

cycle;

Antigen;

```
Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP4_ROTH1
P11198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
   Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                     DOMAIN
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
       ETT
FTT
FTT
FTT
FTT
FTT
FTT
FTT
ST
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDILINE-98437347; Pubmed-9763420;
MEDILINE-98437347; Pubmed-9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Characterization of the kinetochore proteins CENP-F and hBUBRI.";
interactions with the kinetochore proteins CENP-F and hBUBRI.";
j. Cell Biol. 143:49-63(1988).
j. Cell Biol. 143:49-63(1988).
CHROMOSOME SEGREATION DURING MITOSIS. INTERACTS WITH
RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI.
-i- SUBUNIT: HOMO-OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i-SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS), REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.
-i-DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
-i-PTM: HYPERPHOSPHORYLATED DURING MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.; "The C terminus of mitosin is essential for its nuclear localization, centromere/Kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDINE-95319848; PubMed-7651420; MEDINE-95379848; PubMed-7651420; Liu C.-Y., Chen C.-F., Shan B., Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Jones D., Yang-Feng T.L., Lee W.-H.; "Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression."; Moi. Cell. Biol. 15:5017-5029(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE OF 2194-3210 FROM N.A.
MEDLINE-95336446; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
Li Q. and Interpretation of the control of the control
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Breast carcinoma; MEDLINE-95348175; PubMed-7542657; Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.; Liao H., Winkfein R.J., Mack G. Rattner strong protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis."; J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nuclear protein; Centromere; Coiled coil;
                                                                                                                                                                                   F) (Mitosin) (AH
              CENF HUMAN STANDARD; PRT; 3210 AA. p49454; 013246; Q13171; 01-FEB-1996 (Rel. 33, Created) 10-FEB-1996 (Rel. 33, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) CENP-F kinetochore protein (Centromere protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE=95370296; Pubmed=7642639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U19769; AAA82889.1; -. EMBL; U30872; AAA82935.1; -. EMBL; U25725; AAA86889.1; -. HSSP; P02649; LLE4.
                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600236;
                                                                                                                                                                                                                                             antigen).
```

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRKNELEOLKEAFAKEHQEFLTKLAFAEER---NONLML----ELETVQQALRSEMTDNQ 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1006 EREKSISELSDQYKQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNECTSLCE 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 LAGNALYLQK-----TANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFAT--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 -TSKDLSAVS----QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL----FSQEIIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ج</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-280.
MEDLINE-86313706; PubMed-3018754;
MEDLINE-86313706; PubMed-3018754;
Gorziglia M., Hoshino M. 2., Buckler-White A., Blumentals I., Glass R. Flores J., Kapikian A.2., Chanock R.W.;
"Conservation of amino acid sequence of VP8 and cleavage region of
                                                                                                                                                                     LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
(Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                                                                                                                                                                                                                                                                  SSMREWOPCIMTKRPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDILINE=88275070; PubMed=2839714;
Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,
Gorziglia M., Green K., Mishikawa K., Taniguchi K., Jones R.,
Kapikian A.Z., Chanock R.M.;
"Sequence of the fourth gene of human rotaviruses recovered from
"Sequence of the fourth gene of human rotaviruses recovered from
asymptomatic or symptomatic infections.";
T Virol. 62:2978-2984(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946 LLSETLSLEKKEMSSIISLNKREIEELTQENGTLKEINASLNQEKMNLIQKSESFANYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 DLKGSVASLREEI-----RFLTPLAEEVRRLAHNQESLTAAIBELKTIRDSLRDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               (IN REF. 3).
W; 11D83324960E4334 CRC64;
COLLED COIL (POTENTIAL).
                                                                                  OILED COIL (POTENTIAL).
X 177 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                        ER -> DG (IN REF. 3).
L -> Q (IN REF. 3).
D -> N (IN REF. 2).
ELNERVAALHNDGEACK -> S
                                                                                                                                                                                           T -> A (IN REF. 2).
L -> Q (IN REF. 2).
G -> D (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1119 NNSKSEAGGLKQEIMTLKEEQNKMQKEVNDLLQE 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GQLSQLSKTLTSQIALQRKESSDLCSQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / strain 1076)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 124.5;
26.2%; Pred. No. 3.4;
tive 32; Mismatches
                                                                                                                                                                           NUCLEAR I
T -> A (]
                                                                                                                                                                                                                                                                                                                                                                                                                                                   367589 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human rotavirus (serotype 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.23
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                              611
1589
1611
1811
                                                                                                                                                                                                                                                                                                                                                2243
2335
2492
2561
                                 769
1328
1746
2987
2568
2386
2568
3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3210 AA;
                                                                                                                                                                                                                                                                                                                                                                       2335
2492
2545
                                 273
823
1642
1862
2207
2207
2389
                                                                                                                                                                                  3015
```

þ

```
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 FITSLACNALYLOKTAN-LHLYQDLOREVGSLKEINFMLSVLOKEFLHLSKEFATTSK-D 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 FILLVPSNDDYQTPIMNSVTVRQDLERQLGDLRE------EFNSLSQEIAMTQLID 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 LSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 FLTPLAEEVRR---LAHNQESL---TAAIEELKTIRDSLRDEIGQLSQLSKTL-TSQIAL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
84-kDa outer capsid protein among rotaviruses recovered from asymptomatic neonatal infection.", Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).
-1 SUBCELLULAR LOCATION: Outer capsid.
-1 PIM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed-11759840;
Kaneko T. Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watenabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Nakazati N., Shimpo S., Sugimoto M., Matsuno A., Muraki A.,
Yaguda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
Cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                      -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY. PIR; F28839; VPXRW8. PIR; F25904; VPXR16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%; Score 122; DB 1; Length 775;
26.8%; Pred. No. 0.92;
.1ve 33; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                           CAPSID PROTEIN VP4
CAPSID PROTEIN VP8
CAPSID PROTEIN VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EE29A36D36C8018F CRC64;
                                                                                                                                                                                                                                                                                                                                                           N-LINKED GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
ALR4393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 QRKESS--DLCSQIRETLSSPRKSASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : : | : : | OTEGMNFIDISAAVLKTKIDKSTHISPDT 654
                                                                                                                                                                                                                                                                                           OUTER COUTER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                      InterPro: IPR000116; Cap_VP4.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                     775
32
56
97
                                                                                                                  OTHER PRODUCT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
583
606
775 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterla; Cyanobact
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y7J3_ANASP
Q05070;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7J3_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626
  SFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC OCS NEW REAR TRANKER TO SERVICE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial ontities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
              SEQUENCE OF 1-166 FROM N.A.
MEDILINE-9330801; PubMed-8391534;
Well T.-F., Ramasubramanian T.S., Pu F., Golden J.W.;
"Anabaena sp. strain PCC 7120 bifA gene encoding a sequence-specific DNA-binding protein cloned by in vivo transcriptional interference
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 ANLHL------YQDLQREVGSLKEINFMLSVLQK-----EFLHLSKEFATTSK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AILFIADEGLRKGVFELEDIQKDLRQKRE---QLKVAEEQKTQVEIERNKVNOELETTRT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLSAV-----SQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEII 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 DKKQVETQRDQAKKEKLKAQQDLAQTQAQYQRTQSRLGQVVTQYQKAIAELQSVYNQR-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 KALQGAVEQLKTERRRLYAEAKKAIEQRDRELANRQOAIEQRDRELANRQOALQORDQKI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 IASLILIGTIGFLALLGHLVG------FLIAPQITIVLLALFITSLAGNALYLQKT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP4_ROTHN STANDARD; PRT; 776 AA.
01-1199.
01-30L-1990 (Rel. 11, Created)
01-NOV-1990 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
0uter capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 ADLKGSVASLREEIRFLTPLAEEV----RRLAHNQESLTAAIEELKTIRDSLRDEIGQL
                                                                                                                                                                                                                                                                            EMBL; 110036; AaD04182.1; -
Hypothetical protein; Transmembrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88275070; PubMed-2839714;
Gorzigila M., Green K., Nishikawa K., Taniguchi K., Jones R.,
Kapikian A.Z., Ghanock R.M.
"Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
Virol. 62:2978-2984(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 120; DB 1; Length 496;
21.9%; Pred. No. 0.73;
IVe 54; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                POTENTIAL.
HYPOTHETICAL PROTEIN ALR4393.
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
454D67CF420AFB9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human rotavirus (serotype 3 / strain McN13).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBL_TaxID=10955;
                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Pred. No. 0.73.
Live 54; Mismatches
                                                                                                        J. Bacteriol. 175:4025-4035(1993).
                                                                                                                                                                                                                                                             EMBL; AP003596; BAB76092.1; -.
                                                                                                                                                                                                                                                                                                                                                              MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 SQLSKTLTS---QIALQRKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
56375 I
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                              19
496
                                                                                                                                                                                                                                                                                                                                                         496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 57; Conserv
                                                                                            selection.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 57
                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VP4_ROTHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
pp
                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                     g
òγ
                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                      òγ
                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                      ÓΫ
                                                                                                                                                                                                                                                                                                                                                                     589 SVWIDVSEQITGSSDSVRNISTQTSASRRLRLREITTQTEGMNFIDISAAVLKTKIDKST 648
                                                                                                                                                                                                                                                                                                                       QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGF 152
                                                                                                                                                                                                                                                                                                                                                        153 ESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRR---LAHNQESL 209
                                                                                                                                                                                                                                                                                                                                                                                       ---TAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESS--DLCSQIRETLSSPRK 264
                                                                                                                                                                                                                                                                                                                                   492 QDLERQLGDLRE-----FSGI 534
       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                        ( POTENTIAL)
                                                                                                                                                                                  (POTENTIAL)
                                                                                        -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
PIR; G25904; VPXEM9.
Interpro, IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
Coat protein; G1ycoprotein.
                                                                                                                                                                                                                                                                                         8.7%; Score 116; DB 1; Length 776; 25.8%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                  CFCADF4DEE986512 CRC64;
                                                                                                                                           VP4.
VP8.
                                                                                                                                          OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                                                                     (GLCNAC. . .)
                                                                                                                                                                                                            (GLCNAC. . .)
                                                                                                                                                                                                                     (GLCNAC. . .)
                                                                                                                                                                                            (GLCNAC. . .)
                                                                                                                                                                            (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                             (GLCNAC. .
                                                                                                                                                                  N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
60-151-160 (Male-enhanced antigen-2) (MEA-2).
                                                                                                                                                                                                                                                          (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1325 AA.
                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.2; 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-Testis;
MEDLINE-97217683; PubMed-9063644;
                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                        776 AA;
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                               SASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                649 HISPDT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G160_MOUSE
P55937;
                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                Óγ
                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                         FT
FT
FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 IVLEVALQSAKSDKEELDRGAR-RLEEDTEETSGLLEGLRQDLAVKSNQVEHLQGETATL 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 SKDLSAVSQDFYS---CLQGFRDNYKGFESLLDEYKNSTE----EMRKLFSQEII---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : : : : : : : | : : | 1::1 | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTS CAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 VLIALFITSLAGNALYLOKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=90080150; PubMed=2152826; MEDLINE=90080150; PubMed=2152826; Gorzigiia W., Nishikawa K., Hoshino Y., Taniguchi K.; Gorzigiia W. Similarity of the outer capsid protein VP4 of the Gortfried strain of porcine rotavirus to that of asymptomatic human rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01.NOV-1991 (Rel. 20, Created)
01.NOV-1991 (Rel. 20, Last sequence update)
01.NOV-1991 (Rel. 40, Last annotation update)
01.CCT-2001 (Rel. 40, Last annotation update)
01.CCT-2001 (Rel. 40, Last hannaggluthin) (Outer layer protein VP4)
(Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                  DNA SEQ. 7:11-82(1997).

DNA SEQ. 7:11-82(1997).

- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR

- FESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLGGICALLY

TESTIS DEVELOPMENT. HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN

- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN
FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN
EXPIGE CELLS, SPERMATOGONIA, OR SPERMATOCYTES.

- STMILARITY: HIGH, TO HUMAN GOLGIN-160.

- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
"Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 115; DB 1; Length 1325;
21.4%; Pred. No. 4.9;
ive 51; Mismatches 83; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D/oz.v.
HSSP; P18852; 1SCG.
MGD; MGI:96958; Golga3.
MGD; MGI:96958; Developmental protein.
Spermatogenesis; Developmental POLY-ALA.
POLY-ALA.
201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 EELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porcine rotavirus (strain Gottfried).
Viruses, dsRNA viruses; Reoviridae; Rotavirus.
NCBL_TaxID=10917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D78270; BAA19612.1; -.
HSSP; P18852; 1SCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strains.";
J. Virol. 64:414-418(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP4_ROTPG
ID VP4_ROTPG
AC P23045;
```

1

```
MEDLINE-88153889; PubMed-3126192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                 IAPQITIVLLALFITSLAGNALYLQKTAN-LHLYQDLQREVGSLKEINFMLSVLQKEFLH 119
                                                                                                                                                                                                                                                                                                                                                                                                                      463 IAGRESLILL------PSNDDYQTPIMNSVTVRQDLERQLGDLRE------EFNS 506
                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQE---1 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 LSQEIAMTQLIDLALLPLDMFSM-----FSGIKSTIDVAKSMATNVMKKFKKSGLATS 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 IADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                             OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP8.
N-LINKED (GLCNAC...) (POTENTIAL).
SUBCELLULAR LOCATION: Outer capsid. PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE OTHER PRODUCT IS VP5.
                                                                                                                                                                                                                                                                                                                                                                                      36;
                                   SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-91065636; PubMed-2123469;
OSman M., Paz M., Landesman Y., Fainsod A., Gruenbaum Y.;
"Molecular analysis of the Drosophila nuclear lamin gene.";
                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 114; DB 1; Length 77;
23.3%; Pred. No. 3;
tive 41; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 KTLTSQIALQRKES---SDLCSQIRETLSSPRKSASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRLRLREITTQTEGMNFDDISAAVLKTPLDKSTHISPDT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988 (Rel. 09, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622 AA.
                                                                                                                                                               PIR, A33563; VPXRPG
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                        87098 MW;
                                                                                                                                                 EMBL; M33516; AAA47095.1; -.
                                                                                                                                                                                              Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                          240
775
32
56
97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                    247
32
56
97
132
324
583
775 AA;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Ma.
Local 5...
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMO_DROME
P08928;
                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamin DmO.
                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMO_DROME
TO LAMO_DROME
TO LAMO_DROME
DT 01-NOV.
DT 01-FEB.
DT 16-FCT.
DE Lamin 16-FCT.
OC EUKRIYO
OC EUKRIYO
OC EUKRIYO
OC EUKRIYO
OC EDPYDT.
OX NCBI_T?
RR SEQUEN
RX MEDLIN
RX MEDLIN
RY OSMBN 171
RR SEQUEN
RY OSMBN 171
RR SEQUEN
RY MEDLIN
RY SEQUEN
                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                919
SFFF
                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              合
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to incensedisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                        Stuurman N., Maus N., Fisher P.A.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS
MAICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR MEMBRANE,

-I-SUBCELLULAR LOCATION: NUCLEAR ENVELOPE

-I-PUNSTHEE FORMS OF LAMIN HAVE BEEN IDENTIFIED IN D.MELANOGASTER,

-I-PUNSTHEE FORMS OF LAMIN HAVE BEEN IDENTIFIED IN D.MELANOGASTER,

-I-PUNSTHEER FORMS OF LAMIN HAVE BEEN IDENTIFIED IN D.MELANOGASTER,

-I-PUNSTHORY: BELONGY TO THE NUCLEAR ENVELOPE AND IS THEN

PHOSPHORYLATED. FORMING LAMIN DM2.

-I-SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
Gruenbaum Y., Landesman Y., Drees B., Bare J.W., Saumweber H., Paddy M.R., Sedat J.W., Smith D.E., Benton B.W., Flaher P.A.; "Drosophila nuclear lamin precursor Dm0 is translated from either of two developmentally regulated mRNA species apparently encoded by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FARNESYL (BY SIMILARITY).
PSAGPQPPPPSTHSQT -> AIGSAAAAVHSLAD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 TSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S---QDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKL-----FSQEIIADLKGSVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00038; filament; 1.
Pfam; PF00038; filament; 1.
Pfam; PF00932; IF_tail; 1.
Intermediate filament; Colled coil; Nuclear protein; Lipoprotein; DOMAIN 1.
DOMAIN 1. 56 HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R-SEYDAK -> SPQLRVRCQ (IN REF. 1).
DV -> EL (IN REF. 1).
DC8F0187CF2E2A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COIL 2.
HEPTAD CHANGE OF PHASE.
HEPTAD CHANGE OF PHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 112.5; F
24.3%; Pred. No. 2.9;
ative 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REF. 1)
R -> E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKER
                                                                                           jene.";
Biol. 106:585-596(1988).
                                                                                                                                                   REVISIONS TO 24-39 AND 254-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X16275; CAA34351.1; --
EMBL, X07278; CAA30259.1; --
PIR, A29965; A29965.
PIR, A37103; A37103; A37103; ElyBase; FB900002525; Lam.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>..</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
270
622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
409
55
104
242
242
289
3353
619
24
                                                                                         single gene.
J. Cell Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

ŏ g

```
C24700; C24700.
                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
             DDR
KWW
KWW
KWW
FTT
FTT
FTT
FTT
FTT
FTT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILL and A-IV Genes. "

II. and A-IV Genes."

II. and A-IV Genes. "

II. and A-IV Genes."

II. and A-IV Genes."

II. and A-IV Genes. "

III. and A-IV Genes."

III. and A-IV Genes."

III. and A-IV Genes."

III. and A-IV Genes. "

III. and A-IV Genes."

III. and A-IV Genes."

III. and A-IV Genes.

III. and A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84298074; PubMed-6591177; Boguski M.S., Elshourbagy N.A., Taylor J.M., Gordon J.I.; Boguski M.S., Elshourbagy N.A., Taylor J.M., Gordon J.I.; Rata apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segment with amphipathic helical potential."; Proc. Natl. Acad. Sci. U.S.A. 81:5021-5025(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
             TLSRVDLENTIQSLREELSFKDQIHSQEINESRRIKQTEYSEIDGRLSSEYDAKLKQSLQ 269
                                                                                      270 DVRAQYEEQMQINFDEIQSL--IEDKIQRLQEAAARTSNSTHKSIEELRSTRVRIDALNA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87008540; PubMed=3020028; T., Karathanasis S.K.; Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.; Linkage, evolution, and expression of the rat apolipoprotein A-I, III, and A-IV genes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEGINES, BLICKERS, BLICKERS, BLICKERS, BOOGNASS, BOOGNAS, Taylor J.M., BOGUSKI, M.S., Birkenmeier B.H., Elshourbagy N.A., Taylor J.M., Gordon J.I.;
Gordon J.I.;
Freduction of the apolipoproteins. Structure of the rat apo-A-IV grand its relationship to the human genes for apo-A-I, C-III, and E.J. BIOI. Chem. 261:6398-6407(1986).
                                                           184 SL------REEIRFLTPLAEEVRRL----AHNQESLTAAIEELKTIR---DSLRD
                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Apolipoprotein A-IV precursor (Apo-AIV).
                                                                                                                                                                                                                                                                                                         391 AA.
                                                                                                                                                     226 EIGQLSQLSKTLTSQIA-LQRKESSD 250
                                                                                                                                                                                 | : | : | : | : | 328 NINELEQANADLNARIRDLERQLDND 353
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M00002; AAA85909.1; -. EMBL; J02588; AAA40747.1; -. EMBL; M13508; AAA40748.1; -.
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A03095; LPRTA4.
PIR; A25214; A25214.
                                                                                                                                                                                                                                                                                                                  APA4_RAT
                                                                                                                                                                                                                                                                                                                                    P02651;
                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                           APA4_RAT
                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                      DAPPE
```

```
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 FQDKLGNINTYADDLQN-----KLVPFAVQLSGHLTKETERVREELQKELEDLRANMMPH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ANKVSQMFGDNVQKLQEHLRPYATDLQAQINAQTQDMKRQLTPYIQRMQTTIQDNVENLQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEIRFIJPLABEVR-RLAHNQE----SLTAAIEELK-TIRDSLRDEIGQLSQLSKTLTSQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 SS---MVPFANELKEKFNQNMEGLKGGLTPRANELKATIDQNLEDLKSRLAPLAEGVQEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 YLQKTANLHLY-QDLQREVGSLKEINFMLSV---LQKEFLHLSKEFATTSKDLSA---- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             --L 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 (Rel. 11, Created)
0 (Rel. 16, Last sequence update)
11 (Rel. 40, Last annotation update)
14 protein VP4 (Hemagglutinin) (Outer layer protein VP4)
0 outer capsid proteins VP5 and VP8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R., Kapikian A.Z., Chanock R.M. "Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
J. Virol. 62:2978-2984 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 ---VSQDFYSCLQGFRDNYKGFESLLDEYKNS-TEEMRKL---FSQEIIADLKGSVASLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APOLIPOPROTEIN A-IV.
13 X 22 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                8.4%; Score 112; DB 1; Length 391;
11.4%; Pred. No. 1.8;
HSSP; P02671; 1FZB.
InterPro: IRRODA, Apolipoprotein.
Pfam; PF01442; Apolipoprotein; 1.
Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                   24095004A809201D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FITSLAGNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human rotavirus (serotype 1 / strain M37).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IALQ-----RKESSDLCSQIRETLSSPRKSASP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       pred. No. 1.8;
; Mismatches
                                                                                                                                                                                                                                                                                                                       GLU/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=88275070; PubMed=2839714;
                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                                         21.48;
                                                                                                                                                                                                                                                                                                                                                          44456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLIAPQITIVLLAL-----
                                                                            391
330
54
81
103
                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                            391 AA;
                                                                                                                             60
82
115
115
115
115
118
120
225
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (
01-NOV-1990 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP4_ROTHM
P11197;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                    Plasma;
                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
```

,

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODLEROLGDIRE------EFNSLSQEIAMTOLIDIALLPLDMFSM-----FSGI 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 ESLLDEYKNSTEEMRKLFSQE----IIADLKGSVASLREEIRFLTPLAEEVRRLAHNQES 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 LTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKES---SDLCSQIRETLSSPRKS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:: ||:: |:: |-:| |:| |:| |: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    Jones L., Murphy L., McNeil A., Simpson I., Harris D., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · · · ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAR3_SCHPO STANDARD; PRT; 1044 AA. 009857; Q9P7V0; 01-FEB-1996 (Rel. 33, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical 119.1 kDa protein C29E6.03C in chromosome I. SPAC29E6.03C OR SPAC30.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05CA6DDAA258550B CRC64;
                                                                                                                                                                                                                                                                                                                                                 CAPSID PROTEIN VP4. CAPSID PROTEIN VP8. CAPSID PROTEIN VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                     (GICNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 111.5; D
23.2%; Pred. No. 4.4;
Live 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                        OUTER CAPE
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                 OUTER
                  MEDLINE-86313706; PubMed-3018754;
                                                                                                                                                                                                                                                       PIR; E28839; VPXRW7.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87402 MW;
                                                                                                                                                                                                                                                                                                                        Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 ASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 ISPDT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstailon - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                        94 QDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      MCDOUGAIL R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy L., Jones L., McNeil A., Harris D.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 789 ALNDNLGN-----KENIISDLKNK------LSEESTRLQELQSQLNQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 EELKTIRDSL---RDEIGQLSQLSKTLTSQIALQRKESSDLCSQIR-----ETLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamasaki M.;
"A cytoskeleton-related gene, usol, is required for intracellular protein transport in Saccharomyces cerevisiae.";
J. Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                       Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 782-1790 FROM N.A.
Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                     600 1014 COILED COIL (POTENTIAL).
1044 AA; 119127 MW; 52ACE0E174725A59 CRC64;
Rajandream M.A., Walsh S.V.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kendrick K.E., Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
                                                                                                                                                                                                                                                                                                                                                                                8.4%; Score 111.5; DB 1;
21.2%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
11-crecellular protein transport protein USO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1790 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                      EMBL; 266525; CAA91425.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                MEDLINE=91185402; PubMed=2010462;
                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 SPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLEKDLEAATKTA 899
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USO1_YEAST
P25386:
                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USO1_YEAST
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        964 LKSLANN-----YKDMOAENESLIKAVEESKNESSIQLSNLONKIDSMSQEKE 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 NFQIERGSIEKNIEQLKKTISDLEQTKEEIISKSDSSKDEYESQISLLKEKLETATTAND 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ITSLAGNALYLQKTANLHLYQDLQREVGSL-----KEINFMLSVLQKEFLHLSKE-- 123
                                                                                                                            DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL. SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                  nitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil. DOMAIN 1 724 GLOBULAR HEAD.
                                                                              SUBCELLULAR LOCATION: CYTOPEASMIC, ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TAAIEELKTIR---DSLRDEIGQLSQLSKTLTSQIALQRKESSDLCSQIRETLSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEE-VRRLAHNQESL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLED COIL (POTENTIAL).
CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FUNCTION.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FATTSKDLSAVSQDFYSCLQGFRDNYKGFESLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . DEEDDEE (IN REF. 2).
6CE2B216E9FD4818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASP/GLU-RICH (ACIDIC)

G -> E (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

I -> V (IN REF. 2).

I -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 111.5; 22.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0002216; USO1.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                               EMBL; X54378; CAA38253.1; -. EMBL; L03188; AAB00143.1; -. EMBL; U53668; AAB66659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uery Match 8.4 est Local Similarity 22.3 Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1790
487
1790
1786
847
924
1253
1319
1461
1581
                        Bai Y., Symington L.S. Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                              PIR; A38455; A38455
                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P80220; 1DIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924
1253
1319
1461
1581
1600
1661
1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1190 00 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 RK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
6666666666668FFF
```

13

RESULT

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
SPECIFC MAKER THAT, DURING THE DEVELOPMENT OF THE CENTRAL SPECIFC MAKER THAT, DISTINGUISHES ASTROCYTES FROM OTHER GLIAL CELLS.
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92243304; PubMed-1636374; Nishiyama A., Katagiri T., Abe S., Yoshida Y., Washiyama K., Kuwano R., Sakimura K.; Abe S., Yoshida Y., Washiyama K., Kuwano R., Sakimura K.; Filan fibrillary acidic protein (GFAP): molecular cloning of the complete cDMA sequence and chromosomal localization (chromosome 17) of the GFAP gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89296968; PubMed-2740350; Reeves S.A., Helman L.J., Allison A., Israel M.A.; Reeves S.A., Helman L.J., Allison A., Israel M.A.; Molecular cloning and primary structure of human glial fibrillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BEGUENCE FROM N.A.

BEGUENCE 9.0294716.

BEGUENCE 9.029716.

BEGUENCE PROPERTY PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 352-417 FROM N.A.
MEDLINE-89386721; PubMed-2780570;
Medline-89386721; PubMed-2780570;
Medline-89386721; PubMed-2780570;
Medline - Rohmont C.W., Liu N.G., Tourtellotte W.W.;
Changes in brain gene expression shared by scrapie and Alzheimer disease.";
                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glial fibrillary acidic protein, astrocyte (GFAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:5178-5182(1989).
432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17) of the GFAP gene.";
Acta Neuropathol. 83:569-578(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, J04569; AAA52528.1; -. EMBL; S40719; AAB22581.1; -. EMBL; M26638; AAA52529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpretation of the second o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSC-2DPAGE; P14136; HUMAN.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432
104
115
214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intermediate filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A32936; A32936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A60052; A60052.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acidic protein.
     GFAP_HUMAN
P14136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                      HEFFFFF SERVERS SERVER
```

LINKER 12.

```
SEQUENCE FROM N.A.
MEDLINE-88275070; PubMed-2839714;
Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,
Kapikian A.Z., Chanock R.M.;
"Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
J. Virol. 62:2978-2984(1988).
                                                                                                   EMBL; AB007633; BAA24579.1;
EMBL; AF029788; AAC04615.1;
EMBL; Z98762; CAB11475.1;
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; Myosin_N.
InterPro; IPR001609; Myosin_N.
InterPro; IPR001609; Myosin_head.
Ffam; PF00063; Myosin_head; 1.
FRINTS; PR00193; Myosin_N: 1.
PRINTS; PR00193; Myosin_head; 1.
PRNTS; PR00193; Myosin_head; 1.
PRNTS; PR00194; MYOSIN_EAVY.
ProDom; P000355; Myosin_head; 1.
Myosin; Coiled coil; ATP-binding; ACDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VV4_ROTHT STANDARD; P
P11200;
01-UUL-1989 (Rel. 11, Created)
01-NOV-1990 (Rel. 16, Last sequent)
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                             242570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.3:
Best Local Similarity 21.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                 182
686
686
1193
1304
134
1420
2104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1086 AFQNPEKT 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 TLSSPRKS 265
                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                   DOMAIN
NP_BIND
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VP4_ROTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                 82 LYLQKTANLHLXQ------DLQREVGSL-KEINFMLSVLQKEFLHLSKEFA--TT 127
                                                                                                                                                                                                                                                   221 HVELDVAKPDLTAALKEIRTQYEAMASSNMHEAEEWYRSKFADLTDAAARNAELLRQAKH 280
                                                                                                                                                                                                                                     ------LLDEYKN 161
                                                                                                                                                                                                                                                                                                         281 EANDYRRQL-GSLTCDLESLRGTNESLERGMR--EQEERHVREAASYQEALARLEEEGGS 337
                                                                                                                                                                                                                                                                                                                                            219 IRDSLR---DEIGQLSQLSKTLTSQIALQRK-------ESSDLCSQIRETLSS 261
                                                                                                                                                                                                                                                                                                                                                               338 LKDEMARHLQEYQDLLNVKLALDIEIATYRKLLEGEENRITIPVQTFSNL--QIRET-SL 394
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: STABLILIZES THE F-ACTIN CABLES FORMING THE F-ACTIN RING THAT SURROUNDS THE NUCLEUS DURING INTERPHASE. MAY WORK IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98119390.
Motegi F., Nakano K., Kitayama C., Yamamoto M., Mabuchi I.;
"Identification of Myo3, a second type-II myosin heavy chain in the fission yeast Schizosaccharomyces pombe.";
FEBS Lett. 420:161-166(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98062346; PubMed-9398685;
MEDLINE-98062346; PubMed-9398685;
Bezanilla M., Forsburg S.L., Pollard T.D.;
Identification of a second myosin-II in Schizosaccharomyces pombe:
Myp2p is conditionally required for cytokinesis.";
Mol. Biol. Cell 8:2693-2705(1997).
                                                                                                                                                                                                                                                                                 162 STEEMRKLFSQEIIAD---LKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKT
                                                                                                                                              :99
                                                                                                        Similarity 24.4%; Pred, No. 2.3; Onservative 34; Mismatches R6: Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: BINDS TO CDC4 AND RLC1.
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                         86; Indels
                                                                E6C3B3454C3F1250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MXS3_SCHPO STANDARD; PRT; 2104 AA. 014157, 042730, 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) MXO3 OR MYP2 OR SPAC4AB.05C.
                                                                                                                        Pred. No. 2.3;
34; Mismatches
                                                                                                                                                                                                                       128 SKDLSAVSQDFYSCLQGFRDNYKGFES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
                  COIL 2A.
LINKER 2.
COIL 2B.
                                                             49880 MW;
   215
231
253
257
432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    395 DTKSVS 400
                                                                                                                                                                                                                                                                                                                                                                                                        262 PRKSAS 267
                                            DOMAIN
SEQUENCE
                                                                                                      Query Match
                                                                                                                      Local
                              DOMAIN
                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
MYS3_SCHPO
SFFF
                                                                                                                                                                                         g
                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                       윱
                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 YQDLQREVGSLKEINFMLSVLQKEFLHLSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 ESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 IEELKTIRDSLRDEI----GQL------SQLSKTLTSQIALQRKESSDLCSQIRE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2104;
                                                                                                                                                                                                                                                      ATP-binding; Actin-binding; Alkylation.
                                                                                                                                                                                                                                                                    MYOSIN HEAD LIKE.
COILED COIL (POTENTIAL).
ACTIN BINDING (POTENTIAL).
ATKIN BINDING (POTENTIAL).
ALKILATION (BY SIMILARITY).
D -> G (IN REF. 2).
E -> G (IN REF. 2).
E -> K (IN REF. 2).
G -> D (IN REF. 2).
G -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   St. Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human rotavirus (serotype 4 / strain St. Thome
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  774 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 16;
48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 110.5; 21.8%; Pred. No. 16;
```

```
1;
                                                        MEDLINE=86313/06; PubMedF-5018/04;
A Gorzigila M., Hoshino Y., Buckler-White A., Blumentals I., Glass R.,
A Flores J., Kapiklan A.2., Chanock R.M.; Per Conservation of amino acid sequence of vp8 and cleavage region of
a "Conservation of amino acid sequence of vp8 and cleavage region of
a conservation of amino acid sequence of vp8 and cleavage region of
a symptomatic neonatal infection.";
Proc. Natl. Acad. Sci. U. S.A. 83:7039-7043(1986).
C. -- SUBCELLULAR LOCATION: Outer capsid.
C. -- SUBCELLULAR LOCATION: Outer capsid.
C. -- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
PIR, H28839; VPXRAT.
C. -- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
B. RICATO: IPRO00416; Cap_VP4.
C. -- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN VP4.
C. -- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN VP6.
C. -- GABONY COAT PROPER CAPSID PROTEIN VP6.
C. -- CABONY COAT CAPSID PROTEIN VP6.
CARBONY SCI. CARBONY COAT CAPSID PROTEIN VP6.
CARBONY SCI. CARBONY COAT CAPSID PROTEIN VP6.
CARBONY SCI. CARBONY COAT CAPSID CARBONY COAT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588 SEWTDVSEQIAGSSDSVRNISTQTSASRRLRLREITTQTEGMNFIDISAAVLKTKIDRST 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 ESLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRR---LAHNQESL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 ---TAAIEELKTIRDSLRDEIGQLSQLSKTLTSQIALQRKESS--DLCSQIRETLSSPRK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 ODLQREVGSLKEINFMLSVLQREFLHLSKEFATTSK-DLSAVSQDFYSCLQGFRDNYKGF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 QDLERQLGDLRE-----FENSLSQEIAITQLIDLALLPLDMFSM-----FSGI 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.3%; Score 110; DB 1; Length 774;
Best Local Similarity 25.3%; Pred. No. 5.4;
Matches 47; Conservative 31; Mismatches 76; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP8.
N-LINKED (GLCNAC. .) (POTIN-LINKED (GLCNAC. 
SEQUENCE OF 1-280.
MEDLINE=86313706; PubMed=3018754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΜM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1114
1132
1192
277
324
583
606
87455 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 SASPST 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIRPDT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                     FT
FT
FT
FT
FT
FT
SO
```

Search completed: August 13, 2002, 09:30:44 Job time: 380 sec

```
Q9f7t6 chlamydia t
Q9f710 chlamydia t
Q9f712 chlamydia t
Q9f712 chlamydia t
Q9f712 chlamydia t
Q9f7t7 chlamydia t
Q9f7t8 chlamydia t
Q9f7t8 chlamydia t
Q9f7t8 chlamydia p
Q07962 carasius a
Q07962 carasius a
Q07962 carasius a
Q07962 pyrococcus
Q98t96 anguilla ja
Q07488 saccharomyc
P87360 brachydanio
Q1789 homo sapien
Q9f7t8 chlamydia t
Q86200 human rotav
Q90zf7 rana catesb
Q90zf14 human rotav
Q6063 dugesta jap
Q90314 human rotav
Q66bb homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                      Bannantine J.P., Stamm W.E., Suchland R.J., Rockey D.D.;
"Chlamydia trachomatis IncA is localized to the inclusion membrane and Is recognized by antiseara from infected humans and primates.";
EMBL: AF067958; AAC82641.1;
SEQUENCE 273 AA; 30272 MW; E64B846A5D6824EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1333; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 1.6e-81; Matches 273; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                    092828
007962
007962
002428
002478
0014789
09F778
                  Q9PKR8
                          09F7L2
09AM93
09F7K8
09F7T7
046210
                                                                                                                                                                                              09L514
096063
013098
090314
076447
                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-LGV-434;
MEDLINE-99043938; PubMed-9826388;
    069196 PRELIMINARY;
069196;
01-AuG-1998 (TrEMBLEAL: 07,
01-AuG-1998 (TrEMBLEAL: 07,
01-DEC-2001 (TrEMBLEAL: 19,
                                                                                                                                                                                                                                                                                                                                              INCLUSION MEMBRANE PROTEIN.
                                                                            1179
1179
263
3471
471
3259
775
111
1286
644
1931
1931
1931
1940
1740
897
175
 г
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
 RESULT
069196
                                                                                                                                                                                                                                                                                                      å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                              August 13, 2002, 09:30:16 ; Search time 48.57 Seconds (without alignments) 972.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09amb2 chlamydia t
09ama4 chlamydia t
084121 chlamydia t
09ama6 chlamydia t
09am94 chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chlamydia t
chlamydia t
chlamydia t
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O69196 chlamydia t
O9ama5 chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chlamydia t
chlamydia t
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chlamydia chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chlamydia
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the tôtal score distribution.
                                                                                         1333
1 MTTPTLIVIPPSPPAPSYSA......QIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9am94
Q9ama9
Q9f7k9
Q9ama7
Q99q56
Q9ama8
Q9amb0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9amb1
Q9f711
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                       Ltal number of hits satisfying chosen parameters:
                                                                                                                                         562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES

    protein search, using sw model

                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Ligting first 45 summaries
                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9AMA4
084121
Q9AMA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         069196
Q9AMA5
Q9AMB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9AM94
Q9AM49
Q9F7K9
Q9AMA7
Q99Q56
Q9AMA8
Q9RFX7
Q9AMB1
                                                                                                                                                                                                                                                                                                                                     sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                              sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                              sp_rv1rus:*
sp_bacteriap:*
                                                                                                                                                                         Maximum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                     sp_organelle:*
                                                                                   US-09-673-763-14
                                                                                                                                                                                                                                             SP_archea:*
SP_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                Sp_archeap:*
                                                                                                                                                                                                                                                                                                                             sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                       sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                    SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                               sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1000.0
990.6
988.9
988.3
988.3
988.0
998.0
997.9
997.9
                                                                                                                                                                                                                                                            33:
44::
110::
111::
114::
116::
                                                                                        Perfect score:
                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1333
1328
1318
1311
1310
1308
1306
1306
1305
1305
1305
1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                               OM protein
                                                                                                Sequence:
                                                                                                                                         Searched:
                                                                                                                                                                                                                                   Database
                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
```

Gaps

ö

Q9AMA5; Q9AMA5

DE DI

OX OX RR RR RR RT RR SQ

RESULT Q9AMA5

g δ 273;

9 9 240

240

```
pannekock Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A., pannekock Y., van Der Ende A., Eijk P.P., worre S.A., Dankert J.; ossewaade J.M., van Den Fulle A.J.C., Morre S.A., Dankert J.; ossewaade J.M., van Den Fulle A.J.C., Morre S.A., Dankert J.; normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA 147T mutation."; Infect. Immun. 69:4654-4656(2001).

EMBL: AR327010; AA651107.1; SEQUENCE 273 AA; 30346 MW; 7E9F9569405E5469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                        61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                       STRAIN=TW-5;
MEDLINB=21295121; PubMed=11402010;
MEDLINB=21295121; PubMed=11402010;
Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.P.
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Infect normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA 147T mutation.";
Infect. Immun. 69:4654-4656(2001).
EMBL: AR326993; AA6610901:
ERBL: AR326993; AA6610901:
SEQUENCE 273 AA; 30318 MW; 22729569405E422B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MITPILIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                              1 MITPILIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DDC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.6%; Score 1315; DB 2;
ilarity 98.5%; Pred. No. 2.5e-80;
Conservative 2; Mismatches 2;
                                                                                                                                                                                               Query Match 98.9%; Score 1318; DB 2; Best Local Similarity 98.9%; Pred. No. 1.6e-80; Matches 270; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=404-L;
MEDLINE=21295121; PubMed=11402010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, La
01-DEC-2001 (TrEMBLrel. 19, La
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09AMA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09AMA4
                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9AMA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                        δ
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-434/BU;
MEDLINE-21295121; PubMed=11402010;
MEDLINE-21295121; PubMed=11402010;
Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A.,
Pannekoek J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
"Normal Inch expression and fusogenicity of inclusions in Chlamydia
trachomatis isolates with the inch 147T mutation.";
Infect. Immun. 69:4654-4656(2001).
EMBL; AF327009; AAG61106.1; -
EMBL; AF327009; AAG61106.1; -
ENBL; AF327009; AAG61106.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                       (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

99.6%; Score 1328; DB 2;
Best Local Similarity 99.6%; Pred. No. 3.4e-81;
Matches 272; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                          Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                             273
                                                                                             241 IALORKESSDLCSQIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last sem
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                             INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Chlam;
NCBI_TaxID=813;
                                                                                                                                                                                                                                                         01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMB2
Q9AMB2;
```

181

qq

qq

οy

RESULT Q9AMB2

121

g δy

q

οŽ

염

ò

ö

Gaps 9

; 0

Indels

Length 273;

us-09-673-763-14.rspt

```
[4]
STEQUENCE FROM N.A.
STRAIN-SA-1, APACHE-2, IOL-238, UW-36, 2B, 10A, AND 11A;
Pannekoek Y., van der Ende A., Eijk P.F., van Marle J., de Witte M.A.,
Pannekoek Y., van der Ende A., Eijk P.F., van Marle J., de Witte M.A.,
SOSSEWaarde J.M., Morre S.A., van den Brule A.J.C., Dankert J.;
"Normal IncA expression and fusogenicity of inclusions in Chlamydia
trachomatis isolates with the incA 147T mutation.";
SUDMILTERG (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001286; AAC67710.1;
EMBL; AE013466.1;
EMBL; AR279346.
                                                    SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG
               Aravind
                                                                                                                                                                                                                                                                                                                                                                                                                        Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravinc Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., "Baris R.W.;" "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.; "Diverse Mutations in inch Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MT9301;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
"Diverse Mutations in inca Amplified from Clinical Chiamydia
trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 AA; 30327 MW; 6945AE7E8BBBBBF3 CRC64;
                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                         273 AA
                                                                                                              241 IALORKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                               STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF327002; AAG61099 1;
AF327004; AAG61101 1;
AF327005; AAG61103 1;
AF327012; AAG61109 1;
AF327014; AAG61111 1;
AF327015; AAG61111 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF326992; AAG1033.1;
AF32694; AAG61089.1;
AF326994; AAG61091.1;
AF326998; AAG61095.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 273 AA:
                                                                                                                                                                                                                                                                                                        CT119
                                                                                                                                                                                                                 084121
 121
                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                     RESULT
084121
ID 08
AC 08
DT 01
DT 01
                                                                             g
                                                                                                                                                                                                                                                                                                  ö
                                                                                                              ò
                                                                                                                                        a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                        IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                     SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                 SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ 240
                                                                                                                                                                                               Gaps
                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21295121; PubMed=11402010;
Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Normal Inch expression and fusogenicity of inclusions in Chlamydia Lrachomatis isolates with the inch Inf mutation.";
Infect. Immun. 69:4654-4656(2001).
EMBL; AF327008; AAG51105.1;
EMBL; AF327008; AAG51105.1;
SEQUENCE 273 AA: 30265 MW; 2267957C555E572B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                           1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
                                                        SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
       Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 273;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                        Q9AMA6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
    ; DB 16;
4.6e-80;
                            ,,
4
                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.3%; Score 1310; DB 2;
llarity 98.5%; Pred. No. 5.4e-80;
Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                   273 AA.
                         1; Mismatches
                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                          241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
   Score 1311;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                              241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS
98.3%;
98.2%;
                       Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
           Local Similarity
es 268; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-440-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 2699
         Best Loca
Matches
                                                                                                                                                                                                                                                                                                               O9AMA6
                                                                                                                                                                                                                                                                                         9
                                                                                        61
                                                                                                                                     121
                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                        RESULT
Q9AMA6
                                                                g
                                                                                        à
                                                                                                             g
                                                                                                                                  ó
                                                                                                                                                          g
                                                                                                                                                                                                     g
                                                                                                                                                                                 ð
                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

Gaps

0;

Indels

Length 273;

09AM94 Q9AM94

RESULT Q9AM94

g

```
STRAIN-7A, DR. C. 201, 4A, AND 12A;

STRAIN-7A, DR. C. 20, MRC-301, 4A, AND 12A;

PanneNcek Y., van der Ende A., Eijk P.P., van Marle J., de Witte M.A.,

Ssewaarde J.M., Morre S.A., van den Brule A.J.C., Dankert J.;

Ssewaarde J.M., Morre S.A., van den Brule A.J.C., Dankert J.;

Normal IncA expression and fusogenicity of inclusions in Chlamydia

trachomatis isolates with the incA 147T mutation.;

submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AR279354, AAG31149.1;

EMBL, AR279016; AAG61013.1;

EMBL, AR327001; AAG61098.1;

EMBL, AR327001; AAG61108.1;

EMBL, AR327011; AAG61108.1;

EMBL, AR327013; AAG61110.1;

SEQUENCE 273 AA; 30315 MW; 2986A622FIB3BCE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ITPQITIVLALFISLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                           61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                    1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
                                                                                                                                                                                                                                                                                                                                         181 SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                              Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.; "Diverse Mutations in incA Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
61FA8F2085701F58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1306; DB 2; Pred. No. 9.9e-80; 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                   Score 1307; DB 2;
Pred. No. 8.5e-80;
Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 98.0%;
Local Similarity 97.8%;
Les 267; Conservative
   30357 MW;
                                                         98.08;
97.88;
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                          Best Local Similarity
Matches 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
         273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MT5942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
       SEQUENCE
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9F7K9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9F7K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                      Pp
                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                        g
                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                   δy
             တ္ထ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21295121; PubMed-11402010; MEDLINE-21295121; PubMed-11402010; Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A., Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; Normal Inch expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the inch I47T mutation."; Infect. Immun. 69:4654.4656(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IAPQITIVLLALFIISLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAALASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVASLREETRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                 STRAIN-MT9227;
Virsalvosin W.E.;
Virsalvosin W.E.;
Virsalvosin W.E.;
Virsalvosin W.E.;
Virsalvosin W.E.;
Trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARAI1230-1; --
SEQUENCE 273 AA: 30354 MW; 6945AE6AOD5092C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.8%; Pred. No. 7.3e-80;
Matches 267; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                           273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-UW-4;
```

ö

Gaps

;

Indels

Length 273;

09AMA9; 09AMA9 œ

29AMA9

241

181

ò

qq

qq

q δŏ g Qγ

ò

RL SO SO

9

```
MEMBRANE PROTEIN A.
                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                  273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=UW-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 267;
                   NCLUSION
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09AMA8
09AMA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09AMA8
                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID DATE OF THE STANDARD OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Witte M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLING-2129512; PubMed=11402010; Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A Ossewaarde J.M., van Der Ende A.J.C., Morre S.A., Dankert J.; Normal Inch expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the inch I47T mutation."; Infect. Immun. 69:4654(2001). EMBL; AF327007; AGG1104.1; -... SEQUENCE 273 AA; 30337 MW; 6945AE7E8BBB24F3 CRC64;
                                                             SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG
                                                                                                                                            SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                 SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
98.0%; Score 1306; DB 2; Length 273;
Best Local Similarity 97.8%; Pred. No. 9.9e-80;
Matches 267; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  01-00N-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_raxID=813;
                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                        241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                               241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IALORKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  099056
099056;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                     09AMA7;
                                                                                                                                                                                                                                                                                                                                                                Q9AMA7
                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
Q99Q56
ID Q99Q56
AC Q99Q56
DT 01-JUN
DT 01-JUN
                                                                                                                                            181
                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                             Q9AMA7
                     g
                                                           ò
                                                                                                   a
                                                                                                                                       à
                                                                                                                                                                             a
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
de Witte M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           1 MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTTPTLIVIPPSPPAPSYSANRVPOPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.P. Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; Normal Inch expression and fusogenicity of inclusions in Chlamydia Lrachomatis isolates with the inch IIT mutation."; Infect. Immun. 69:4654-4656(2001).

EMBL; AF327005; AAG5102.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                     SEQUENCE FROM N.A.
STRAIN-MT9309, AND MT9309;
STRAIN-MT93109, AND MT9309;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
"Diverse Mutations in incA Amplified from Clinical Chiamydla trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF327331; ARXI1235.1;
EMBL, AF327330; AAXI1235.1;
                                                                                                                                                                                                                                                                                                                          Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                        30339 MW; B445B3638B8BEBE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     005; AAG61102.1; -.
273 AA; 30387 MW; 6945AE7E9B8AEBF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                   Score 1305; DB 2; 1
Pred. No. 1.2e-79;
1; Mismatches 5;
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1305; DB 2;
Pred. No. 1.2e-79;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21295121; PubMed-11402010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -;
                                                                                                                                                                                                                                                                                                                      97.98;
97.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%;
ilarity 97.8%;
Conservative 1
                                                                                                                                                                                                                                                                                                                   Query Match 97.9
Best Local Similarity 97.8
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
```

ö

```
STRAIN-MT-566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AMB1;
01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMB1
                                                                                                                                                                                                                                                                                                                                                                                             Q9AMB0
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9AMB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                 RESULT 14
Q9AMB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                           181
                  61
                                                                                                     121
                                                            121
                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                        g
                                                                                                                                                                                                                                         δ
                                                              δ
                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=D(S) 2923;
MEDLINE-20072706; PubMed=10603409;
Suchland R.J., Rockey D.D., Bannantine J.P., Stamm W.E.;
Suchland S.Chlamydia trachomatis that occupy nonfusogenic inclusions
lack IncA, a protein localized to the inclusion membrane.";
Infect. Immun. 68:360-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-IC-CALB;
Pannekoek Y., van der Ende A., Eijk P.B., van Marle J., de Witte M.A., Ossewaarde J.M., Morre S.A., van den Brule A.J.C., Dankert J.;
Normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA 147T mutation.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1637733; AAD48440.1;
EMBL, AF132733; AAG61993.1;
EMBL, AF326996; AAG61993.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                              240
                                         IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                              61 IAPQITIVLALAIFIISLAGNALYLQKTANLHIYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
MTTPTLIVTPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL 60
                                                                                                                                                                                                                                              SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MT9346, MT9334, MT9291, AND MT9336;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
"Diverse Mutations in incA Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9D0C862A533FDE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1302; DB 2; Pred. No. 1.8e-79; 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                      241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK11231.1; -. AAK11232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG61096.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.7%;
Best Local Similarity 97.4%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF327332; AAF
CE 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF326999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF327328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29RFX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9RFX7
                                                  61
                                                                                                                                                                                                                           181
                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                RFX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LID DTT ACCOON ON SERVICE REPORTS AND SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA RA RA RA DR DR DR DR DR DR SO SO
                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                       Q
                                                                                                                                      Qγ
                                                                                                                                                                             g
                                                                                                                                                                                                                         δ
      g
                                                  δ
```

```
pandekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A., Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; "Normal Inca expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the inch 147T mutation."; Infect. Immun. 69.4654.4656(2001).

EMBL; AF326997; AAG61094.1; AGG1094.1; AGG1094.10890F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IAPQITIVLLALFITSLAGNALYLQKTANLHLYQDLQREVGSLKEINFMLSVLQKEFLHL 120
                                                                                                                                                        180
                                                                                            180
                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTTPTLIVIPPSPPAPSYSANRVPQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVGFL
SVASLREEIRFLTPLAEEVRRLAHNQESLTAAIEELKTIRDSLRDEIGQLSQLSKTLTSQ
                                                        SKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFESLLDEYKNSTEEMRKLFSQEIIADLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1293; DB 2;
Pred. No. 7.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                    241 IALQRKESSDLCSQIRETLSSPRKSASPSTKSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21295121; PubMed-11402010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.0%;
nilarity 97.4%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                               INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
```

```
ö
                  Gaps
                                                                        ö
                                                           Ouery Match
Best Local Similarity 97.4%; Pred. No. 8.5e-79;
Matches 266; Conservative 1; Mismatches 6; Indels (
      Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                              INCLUSION MEMBRANE PROTEIN A.
g
                                                                                      δ
                                                                                            q
                                                                                                 ò
                                                                                                         원. ở
                                                                                                                     q
                                                                                                                              à
```

Search completed: August 13, 2002, 09:30:17 Job time: 373 sec

pi.

•

OM protein - protein search, using sw model

August 13, 2002, 09:22:24; Search time 29.79 Seconds (without alignments) 1145.073 Million cell updates/sec Run on:

US-09-673-763-8 1733 1 MTVSTDNTSPVISRASSPTF......DDSAQPQDENQSDAGEHKDS 355 Title: Perfect score: Sequence:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Atal number of hits satisfying chosen parameters:

nimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	inclusion membrane hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable inclusion hypothetical prote protein Kinase (EC microtubule bindin early endosome ant spindle pole body outer membrane pro kinasin-like spind chromosome segrega structural mainten methyl-accepting c kinasin-like spind chromosome segrega structural mainten methyl-accepting c kinasin-like spind chromosome segrega structural minen myosin II heavy ch hypothetical prote hypothetical prote citron - mouse skeletal myosin - paramyosin - fluke hypothetical prote myosin heavy chain male-enhanced anti apsB protein - Eme myosin heavy chain	
SUMMARIES	S61491 A72108 B86514 B86514 B86514 B86514 B86514 C71553 C71553 C71553 T13030 T13030 T13030 T13030 T13030 T147237 AC2675 AC2675 AC2675 AC2675 AC2675 AC2675 AC2675 AC2675 AC2675 AC2675 T122976 S68420 S68420 T122976 S68420 T122976 S704090 AC2675 T122976 T122976 T122976 T122976 T122976	
DB		
Length I	355 390 273 273 273 273 273 1733 1733 1165 1165 1165 1165 1165 1165 1165 11	
& Que Mat	0001 1111 1011	
	1733 2000 1800 1800 1850 1850 1860 1800 1800 1800 1800 1800 1800 180	
Result No.	22222222222222222222222222222222222222	

RESULT 2
472108
472108
hypothetical protein CP0581 [imported] - Chlamydophila pneumoniae (strains CWL029 and C. Species: Chlamydophila pneumoniae (species: Chlamydophila pneumoniae, C. Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C. Accession: A72108; B81560

Htrl6 transducer	atorout troublett	M protein - profesion	methyl-soconting	CODSGRAGG PURCEBOT	hypothetical arets	transdicer protets	hypotherical coile	transducer protects	probable chemotest	Synaptonemal compl	probable nuclear n	d table of about	hynothetical prote		methyl-accepting c
F84219	S67593	C64527	F72288	F75103	T33318	T44989	T38077	T44258	F71161	S49461	T41023	S21801	F71980	C72291	D96954
N	ď	~	~	~	7	N	7	a	a	~	C)	_	~	~	~
628	1790	284	539	880	1475	773	1957	423	739	993	1837	1999	327	530	569
7.8 628	7.7 1790	7.7 284	7.7 539	7.7 880	7.6 1475	7.6 773	7.6 1957	7.6 423	7.6 739	7.6 993	7.6 1837			7.6 530	
134.5 7.8 628	7.7	133.5 7.7 284	133 7.7 539	133 7.7 880	132.5 7.6 1475	132 7.6 773	7.6	7.6	7.6	131.5 7.6 993	7.6			7.6	

ALIGNMENTS

RESULT 1 Solidation membrane protein A - Chlamydophila psittaci C; Species Chlamydophila psittaci R; Rockey, D.D; Henizen, R.A.; Hackstadt, T. Wol. Liolning and Characterization of a Chlamydia psittaci gene coding for A; Reference number: S61491; MuID:95302975 A; Recence number: S61491; MuID:95302979 A; Recence number: S61491; MuID:96302980PREREAGERERESCENCAMESTERESCENCE		a pro		; 0												
SEULT 1 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.Mar-2000	coding for	9516599	Gaps											55	55
SEGULT 101491 Columnary Maccies 27 Accessic Acce	t_change 31	ittaci gene		Length 355; Indels 0;	AVGAKTAIEPEC	AVGAKTAIEPEC	MLVSFVIVITA		CLHTRLSDFGDF		DEAVQAMMSSVT		STLSHSIATLQE			
SEGULT 101491 Columnary Maccies 27 Accessic Acce	psittaci psittaci r-1997 #tex	hlamydia ps		3; DB 2; 4.3e-93; hes 0;	ISIEAPTSSAA 	ISIEAPTSSAA	STPSLILMLAI	STPSLILMLAI	/ELSEQINQLK	FLSEQINOLK	(LAQSLKETFS)		KRKQELEEAC		DDSAQPQDEN	DDSAQPODEN
SEGULT 101491 Columnary Maccies 27 Accessic Acce	lamydophila Chlamydia ision 13-Ma	ckstadt, T. Slon of a Cl	IID:9516598	Score 173: Pred. No.	KDFDNNKIIP	KDFDNNKIIPI	LVCLYLGSVIE	TACLYLGSVIS	TAVENLKAVNV	TAVENLKAVNV	KVETMLSPFEK	KVETMLSPFEK	OLREEQVRFLE		AESSTVEEASQ	AESSTVEEASQ
SEGULT 101491 Columnary Maccies 27 Accessic Acce	ein A - Chl a psittaci, quence_revi	R.A.; Hac -626, 1995 Mracterizat 191; MUID:9		 	ASSPIFGDHG	ASSPTFGDHG	IALFVVGIAA	IALFVVGIAA	OFGEENTRLH	OFGEENTRLH'	SLEEFKSVGT	SLEEFKSVGT	TVIEQLKADA	IVIEQLKADA(RLIGVMVQDGA	
SEGULT 101491 Columnary Maccies 27 Accessic Acce	nbrane protu hlamydophila pr-1996 #sec Sf-1491	D.; Heinzen, 15, 617, 11ng and channer: S61491	eliminary 7pe: DNA 1-355 <roc> cences: EMBI</roc>	ı Similarity 55; Conserv	STDNTSPVISE	STDNTSPVISE	RICYLVKIIAA	RICYLVKIIAA	QVVRHMKQQIQ	QVVRHMKQQIQ	DFTALIADFOL		NALKELITENK	NALKELITENK	DSTTNLHAVES	DSTINLHAVES
RESULT 501491 10Clustic C;Date: C;Date: C;Date: C;Date: C;Date: M,Title M,Title A;Gross A;G	1 on mer es: Cl 27-Al	y, D.I crobic : Clor ence r	s: pre ale ty nes: 1	Match Socal												
See	SULT 1491 clusi Speci	Rocke 1. Mi Fitle Refere	Status Molecu Residu Cross	luery Best I Matche			v	w	12	12	18	18	24	24	30	30
	88.40.00.00.00.00.00.00.00.00.00.00.00.00.	A A A A	AAAA	. • • •	Š d	2	οy	qq	Qy	QQ	Qγ	QQ	Οy	qq	QY	Q

13;

Gaps

38

212

265

```
inclusion membrane localised protein IncA TC0396 [imported] - Chlamydia muridarum (st inclusion membrane localised protein IncA TC0396 [imported] - Chlamydia muridarum, Chlamydia trachomatis MoPn C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C; Accession: H81707
R; Read T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke R; Red T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Kolonay, J.; McClarty, G.; Salzbe, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A; Reference number: A81500; MUID:20150255
A; Residues: 1-276 <TET>
A; Molecule type: DNA
A; Residues: 1-276 <TET>
A; Residues: 1-276 <TET>
A; Cienetics: A; Cienetics: Strain Nigg (MoPn)
C; Genetics: A; Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKEL---- 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LVKIIAAIALFVVGIAALVCLYLĢSVIS-----TPSL-ILMLAIMLVSFVIVITAIRDGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TSPVISRASSPTFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AIALFVVGIAALVCLYLGSVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVRHMKQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ::| |:: :| :: :| ::| ::| 50 -AILSIIGFLAILGHAIGFLIAPQVALVLIAVFIISLLGNALYLCKTAPLRLYKELQQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSPTFGDHGKDFDNNKIIPISIEAP--TSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TSPTLVE------MPLSCYPPTHTSSTACTKRSSSLYKPSLIETVQRVAAFVSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASLKEVNFL-----VSLDFHNLLQDFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGEERRLREEVSRFTSENQRLTVITTLETEVKDLKAAKDQLTLEIEAFRNENGNLKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LREEQVRFLEKRKQELEEACSTLSHS1ATLQESTTLLKDSTTNLHAVESRL1GVMVQDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTRVVGELLESENKLSQACSALRQEIEKLAQHETSLOORIDAMLAQEONL-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKS-VGTKVETMLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| || :: : : : : | | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 FEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELI-----TENKTVIEQLKADAQ
                                                                                                                                                                                                                                                                                                                                                                          ----IPIPAPTTP----GIPTT----KPRSSFIEKVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 276;
                                                                      Length 390;
                                                                                                                                                                                  Indels
                                                                11.5%; Score 200; DB 2; L¢
ilarity 23.0%; Pred. No. 0.00015;
Conservative 64; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 185; DB 2;
Pred. No. 0.00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PSQVVRHMKQQIQQFGEEN----TRLHTAVENLKAVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Sccilarity 23.4%; Pre
Conservative 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | : :: : |
EQVTALEKMKQEAQKAESE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                            Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                               SSPVNNTPSAPN-
                                                                                                 Query Match
                                                                                                                                                 Best_Local
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                         ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ë
                                                                                                                                                                                                                                                                        A.Molecule type: DNA
A.Residues: 1-390 cARN>
A.Residues: 1-390 cARN>
A.Gross-references: GB:AE001605; GB:AE001363; NID:g4376455; PIDN:AAD18339.1; PID:g437645
A.Experimental source: strain CWL029
A.Experimental source: strain CWL029
A.Experimental source: strain CWL029
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A.Fitle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A.Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g7189493; PIDN:AAF38399.1; PID:g71894
     ρ.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K.; Shiba, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
B86514
hypotherical protein CPj0186 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: B86514
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: Preliminary
A;Wolecule type: DNA
A;Gross-references: GB:BA000008; NID:g8978559; PIDN:BAA98396.1; GSPDB:GN00142
C;Genetics:
A;Gene: CPj0186
Fan, J.; Olinger, L.; Grimwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| | | :: | | :: | : : | | :: | : | | :: | : | | :: | | :: | :: | | :: | : | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKS-VGTKVETMLSP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QALKVLLGQEWVQEAQTHVKAMQEQIQALQAEILGMHNQSTALQKSVENLLVQDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TENKTVIEQLKADAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTRVVGELLESENKLSQACSALRQEIEKLAQHETSLQQRIDAMLAQEQNL----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 TSPVISRASSPTFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---IVAKYILFAI----AATSGALGTILGLSGALTPGIGIALLVIFFVSMVLLGLILKDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 LVKIIAAIALFVVGIAALVCLYLGSVIS----TPSL-ILMLAIMLVSFVIVITAIRDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGEERRLREEVSRFTSENQRLTVITTLETEVKDLKAAKDQLTLEIEAFRNENGNLKTT
     R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 PSQVVRHMKQQIQQFGEEN-----TRLHTAVENLKAVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 200; DB 2;
Pred. No. 0.00015;
!; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 FEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Molecule type: DNA
A; Mosidues: 1-390 <a href="https://www.nes.nda.ha.cross-references">https://www.nda.ha.cross-references</a>: GB: AE00217; GB: AE002161;
A; Cross-references: GB: AE002217; GB: AE002161;
Aperimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 200; 23.0%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQVTALEKMKQEAQKAESE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CPn0186; CP0581
                                                                                                                                                                                                                             A; Accession: A72108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
```

g ōλ ΩD ŏ ρp δŻ q

δλ g δÿ g

g

δ

11;

Gaps

49 73

m

;

Gaps

32;

```
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C; Keywords: ATP; phosphotransferase P;75-343/Domain: protein kinase homology <KIN>F;1013-1062/Domain: protein kinase C zinc-binding repeat homology <KZN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 QVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTG 183
                                                                                                                                                                                                              251 QAVEDLGLALDSLEERVGDLEFAVEDL---TLQLSSLDSRVGALEDRVADIEGRLEAVEG 307
                                                                                                                                                                                                                                                          DF-----TALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQ--EAVQAMMS 234
                                                                                                                                                                                                                                                                                    1: 1 | 1: 1: 138 SLEDLSGAVDAMSQQLQALASEDLESLSSRVEDL----EARVGSVEDRLSQAEEDIDSLTT 363
                                                                                                                                                                                                                                                                                                                                                                                                             295 LQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVE-----EASQDDSAQPQDENQSD 348
                                                                                                                                                                                                                                                                                                                                     SVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIAT 294
                                                                                                                                                                                                                                                                                                                                                                 424 LQAEVETLQQSIVE---IDRRL------GQLRSTVDAVRLEVESLGEKLVQAEEKNQRQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL-- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELE---EACSTLSHSIATL--- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QESTILLKD-----STINLHAVESRLIGVMVQD--GAESSIVEE--ASQDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1732;
                                                                                                                      Length 533;
                                                                                                              8.6%; Score 149; DB 2; Length 53
24.0%; Pred. No. 0.2;
.ive 46; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
8.4%; Score 145.5; DB 2;
Best Local Similarity 21.1%; Pred. No. 1.3;
Matches 54; Conservative 59; Mismatches 114;
                A; Experimental source: strain K1
C; Genetics:
A; Gene: APE1216
                                                                                                          Ouery Match
Best Local Similarity 24.08,
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1
474 DASIED 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 AGEHKD 354
                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                                      õ
                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                   gg
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                  probable inclusion membrane protein A - Chlamydia trachomatis (serotype D, strain UW3/Cx C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: C3-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, A:Tile: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trace Accession: C71553
                                                                                                                                                                                                                                                                                                                                                                                                                       A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-273 <ARN>
A.Cross-references: GB.AE001286; GB.AE001273; NID:93328516; PIDN:AAC67710.1; PID:9332851
A.Experimental source: serotype D, strain UM-3/Cx
C;Genetics:
A;Gene: incA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UV.2553

UV.2552

UV.2552

C;Species: Aeropyrum pernix

C;Species: Aeropyrum pernix

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999

R;Kawarabayasi, Y: Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

B;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

B;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, J.; Kudoh, Y.; Yamazaki, J.; K

B;Attle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A;Accession: G72593

A;Attle: Dianarayasion: G72593

A;Status: prellininary

A;Molecule type: DNA

A;Residues: 1-533 <KAW>

A;Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BAA80205.1; PID:d1043991; PID:g510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                            208 RRLAENKEDLLKIVQDLQDIRDK----RAEINNLSQASKTLSEQIASQIEENEKLYANI 263
92 SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ITENKTVIEQLKADAQ-LREEQVRFLEKRKQELEEACSTLSHSIAT-LQESTTLLKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| :: ::: || | : || || : || || SLLDEYKNSTEEMRKLFSOEITADLKGSVASLREEIRFLTPLAEEVRRLAHNQOSLTVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQLKA-DAQLREE--QVRFLEK-----RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 164.5; DB 2;
22.8%; Pred. No. 0.011;
tive 59; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                          306 TTNL 309
                                                                                                                                                                TKAL 267
                                                                                                                                                                264
              155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214
                                                                                  a
                                                  ò
                                                                                                                      ò
                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

effec

as a Cdc42

ï

```
spindle pole body protein NUF1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D9476.3; protein YDR356w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 07-May-1993 #text_change 23-Mar-2001
C;Accession: S26710; S34288; A49455; S61152
C;Accession: C.; Copeland, C.S.; Snyder, M.
J. Cell Biol. 116, 1319-1332, 1992
A;Title: The NUF1 gene encodes an essential coiled-coil related protein that is a pot A;Reference number: S26710; MUID:92176232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: 340/10
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-544 (AUIR)
A; Residues: 1-544 (AUIR)
A; Residues: 1-544 (AUIR)
A; Cross-references: EMBL:211582; NID:94069; PIDN:CAA77668.1; PID:94070
A; Cross-references: EMBL:211582; NID:94069; PIDN:CAA77668.1; PID:94070
A; Note: the authors translated the codon GAG for residue 206 as Asp and CTG for residue
A; Note to the EMBL Data Library, June 1993
A; Description: A spacer element in the Saccharomyces cerevisiae spindle pole body who A; Reference number: 534287
A; Accession: 534288
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-944 (KIL)
A; Cross-references: EMBL:X73297; NID:9312173; PID:9312175
A; Cross-references: EMBL:X73297; NID:9312173; PID:9312175
A; Cross-references: EMBL:X73297; NID:94064779
A; Title: A spacer protein in the Saccharomyces cerevisiae spindle pole body whose translation and the complex of the
                           A; Accession: $44243
A; Status: prellminary
A; Status: prellminary
A; Mondecule type: mRNA
A; Residues: 1-254, C'. 256-257, LQ', 260-276, A', 278-283, 'A', 285-519, 'D', 521-574, 'EQ', 5.
A; Cross-references: EMBL: X78998; NID:9475933; PIDN:CAA55632.1; PID:9475934
C; Genetics:
A; Gene: GDB:EEA1
A; Cross-references: GDB:1369996
C; Superfemily: human early endosome antigen 1
C; Superfemily: human early endosome antigen 2
C; Keywords: calmodulin binding; endocytos1s; metal binding; peripheral membrane prote
                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 MKQQIQQFGEE-----NTRLHTAVENLKAVNVELSEQINQLKQLHTRLSBFGDRLEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 LE-KRKQELEBACSTLS---HSIATLQ----ESTTLLKDSTTNLHAVESRLIGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 NTGDF-----TALIADFQLSLEEFK-SVGTKVETMLSPFEKLAQSL-KETFSQEAVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LRTNLNALKELITENKTVIEQLKADAQLREEQVRF
                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                           Length 1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1995
A; Description: The sequence of S. cerevisiae cosmid 9476.
                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 143; DB
24.0%; Pred. No. 1.4;
Live 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1048 DLKSVEEKLSLAQEDLISNRNQIGNQN 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 ESSTVEE---ASQDD--SAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL:X73297
                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.3%
Best Local Similarity 24.0%
Matches 64; Conservative
S44243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-22 <KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMSSVTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   early endosome antigen 1 - human
N.Alternate names: endosome-associated protein
N.Alternate names: endosome-associated protein
C; Species: Homo sapiens (man)
C; Date: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 10.Sep-1999
C; Accession: A57013; S44243
R; Mu, F.T.; Callaghan, J.M.; Steele-Mortimer, O.; Stenmark, H.; Parton, R.G.; Campbell, R; Mu, F.T.; Callaghan, J.M.; Steele-Mortimer, O.; Stenmark, H.; Parton, R.G.; Campbell, A; Title: EEA1, an early endosome-associated protein. EEA1 is a conserved alpha-helical 1, A; Reference number: A57013
A; Mocession: A57013
A; Accession: A57013
A; Molecule type: mRNA
A; Residues: 1.1410 <RES>
A; Cross-references: GB:L40157; NID:g1016367; PIDN:AAA79121.1; PID:g1016368
B; Seelig, H.P.
submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1297 AKLSGELQQVQEANGDIKDSLVKVEELVKVLEEKLQAATSQLDAQQATNKELQELLVKSQ 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1117 VEAIQVANANISATNAELSTVLEVLQAEKSETNHIFELFEMEADMNSERLIEKVTGIKEE 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 IKNLQEEVTKAKTENLELSTGTQTTIKDLQERLEITNAELQHKEKMASEDAQKIADLKTL 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335
                                                                                                                                                                                                            microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Spate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TFSQEAVQAMMSSVTEL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- EE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SEQINQLKQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 STLSHSIATLQESTTLLKDSTTNLH----AVESRLIGVMVQDGAESSTVEE----ASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QLKADAQ-LREEQVRFLEKRKQE--LEEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --HTRLSDFGDRLEANTGDFTALIADFQLSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRHMKQQIQQFGEENTRLHTAV-----ENLKAVNVEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145; DB Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain Oregon R G;Genetics:
A;Cross-references: FlyBase:FBgn0020503
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKSVGTKVETMLSPFEKLAQSLKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.4%; Scc
20.6%; Pre
tive 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RINLNALKELITENKTVIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                            :: |:||: |::
744 EKTRRESQSEREEFEN 759
                           339 AQPQDENQSDAGEHKD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1357 ENEGNLÖGES 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 DDSAQPQDEN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                   C; Accession: T13030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                    οy
                                                                                        Db
```

```
methyl-accepting chemotaxis protein VCA1056 [imported] - Vibrio cholerae (strain NJE9 C; Species: Vibrio cholerae
C; Species: Vibrio delay chole
                                     146 QSDELQSLDAKVNEALSKIAALESKLSGDFVNKDYVDSKIAQTVSKLSDLEGRLSAVETK 205
                                                                                     182 TGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRT 241
                                                                                                                                                                                    242 NLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTL 301
                                                                                                                                                                                                                       Kinesin-like spindle protein HKSP - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: G02157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 LVKIIAAIALFVVGIAALVCLYLGSVISTP--SLILMLAIMLVSFVIVITAIRDGTP--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 IMKVLIAIVIGAV-IATLAAWAVGNGISKPIRDSISQIQRMSRDNDLTVRLSEQGSDEIR 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 -----SQVVRHMKQQIQQFGEE----NTRLHTAVENLKAVNVELSEQ------IN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 QLKQLHTRLSDFGDRL----EANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 EMSASITEVSEFAQRAATFVQEANQKGHGGVSVGNELA-RDMTSIN---OOMASAVEAIA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 LREEQVRF----LEKRKQE----LEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLI 317
                                                                                                                       QSLKETFSQEAVQAMMSSVTELRTNLNALKELITENKT------VIEQLKADAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 770;
                                                                                                                                                                                                                                                                                       LKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQSDA 349
                                                                                                                                                                                                                                                                                                                      8.1%; Score 140; DB 2; L
21.6%; Pred. No. 1;
Live 60; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GVMVQDGAESSTVEEASQDDSAQPQDEN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 QIATATEQQRGVTEEINANITSISDVSASVTVQVGEVN 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.69
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
G02157
                                                                                  ò
                                                                                                                            qq
                                                                                                                                                                               ò
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
A;Residues: 1-403 <arn>
A;Cross-references: GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AAD36794.1; PID:g498230
C;Genetics:
A;Gene: TM1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72216
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 LEANTGDFTALIADFQLSLEEFK-----SVGTKVETMLSPFEKLAQSLK----ETFSQ- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 MKQQIQQFGEENTRLHTAVENLK------AVNVELSEQINQLKQLHTRLSDFGDR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : : .| :| :| :| :| :| .434 BRIIDLQKKVKQLENDLFVKTHSESKTITIDNELESKDKLIKILENDLKVAQEKYSKME 493
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 KVSTLEDLVSTALMKVQNLSDNFGGVTSDLETLKNDVANLKATLVDLKNLRVEVMSQVQS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 VGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLGSVISTPSLILMLAIM 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 FGEE----NTRLHTAVENLKAVNVELSEQI-----NQLKQLHTRLSDFGDRL---EAN 181
A;Reference number: S61148
A;Accession: S61152
A;Molecule type: DNA
A;Residues: 1.94 4 cDUZ>
A;Cross_references: EMBL:U28372; NID:9849170; PID:9849173; MIPS:YDR356w
A;Gene: SGD:NUF1; SPC110
A;Gene: SGD:NUF1; SPC110
A;Gross_references: SGD:S0002764; MIPS:YDR356w
A;Map position: 4R
C;Keywords: coiled coil; microtubule; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAVQAMMSSVTELRTNLNALKELITENKTV------IEQLKADAQLREEQVRFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 KRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQ
                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 403;
                                                                                                                                                                                                                                                                                                                              Length 944;
                                                                                                                                                                                                                                                                                                                      Score 141; DB 2; Length 94
Pred. No. 1.1;
6; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVSFV--IVITAIR------DGTPSQV-----VRHMK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.1%; Score 140.5; DB 2;
Best Local Similarity 21.0%; Pred. No. 0.44;
Matches 73; Conservative 75; Mismatches 113;
                                                                                                                                                                                                                                                                                                                 8.1%; Scor
23.5%; Pred
ative 56; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENYEKQLESLRKDIEEYKES 566
                                                                                                                                                                                                                                                                                                                                                                    61; Conservative
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tatus: preliminary
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Si
Matches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
H72216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ç

ò

13;

```
structural maintenance of chromosome protein homolog smc (AF172724) [imported] - Agrostices aprobacterium tumefaciens 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 c; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 c; Accession: A97457 accession: A97457 b.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm R; Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001 at pathogen and Biotechnology Agent Agrobacterium A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Accession: A97359; PMID:11743194 a; Ascession: A97457 a; Status: preliminary A; Molecule type: DNA A; Mosession: A97457 a; Baseidnes 1-116, Arma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1165 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86610.1; PID:g15155782; GSPDB:GN00169
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EAAÄGRÖQLERAIRDLSDRKLRLERQSQEASAEI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 --DRLEANTGDFTALLADFQLSLEEFKS-VGTKVETMLSPFEKLAQSLKETFSQEAVQAM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 REERLVADNAQILARLDEEBRELLDILSDSGRHADEMREAFEAAAVKLAES-----EAV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 KQQ-----IQQFGEENTRLHTAVENLKAVNVELSEQINQL----KQLHTRLSDFG---- 175
                                                                                                                                                         383
                                                                                                                                                                                                                 233 MSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSI 292
                                                                                                                                                                                                                                                                             ---EAAAGRQQLERAIRDLSDRKLRLERQSQEASAEI 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
233 MSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSI
                                                                                                                                                     330 REERLVADNAQILARLDEEEAELLDILSDSGRHADEMREAFEAAAVKLAES-----EAV
                                                                                             176 -- DRLEANTGDFTALIADFQLSLEEFKS-VGTKVETMLSPFEKLAQSLKETFSQEAVQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATLQESTTLLKDSTTNLHAVESRLIGV----MVQDGAESSTVEEASQDDSAQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 ATLQESTTLLKDSTTNLHAVESRLIGV----MVQDGAESSTVEEASQDDSAQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%; Score 140; DB 2;
25.0%; Pred. No. 1.6;
tive 35; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: August 13, 2002, 09:24:53
ne: 149 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: AGR_C_1466
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.1%
Best Local Similarity 25.0%
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 FISITAERA---
                                                                                                                                                                                                                                                                                                     384 FTSITAERA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                g
                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosome segregation protein [imported] - Agrobacterium tumefaciens (strain C58, Dupon Species: Agrobacterium tumefaciens ate: 11-Jan-2002 #text_change 11-Jan-2002 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Status: preliminary
A;Molecule type: DA
A;Molecule type: DA
A;Residues: 1-1155 < KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41817.1; PID:g17739174; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; PMID:11743193
A;Accession: AC2675
                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-1056 <WHI>
A;Cross-references: EMBL:U37426; NID:91171152; PIDN:AAA86132.1; PID:91171153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 KQQ----IQQFGEENTRLHTAVENLKAVNVELSEQINQL----KQLHTRLSDFG---- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 EEACSTLSHSIATLQES--TTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD--- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 VITAIRDGTP-----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                              C)Generics:
A)Gene: GDB:KNSL1; EG5; KSP
A)Gene: GDB:RNSL1; EG5; KSP
A)Gene: GDB:RNSL1; EG5; KSP
A)Gross-references: GDB:132856; OMIM:148760
A)Map position: 10q24.1-10q24.1
C)Superfamily: kinesin-related protein EG5; kinesin motor domain homology
C,Superfamily: kinesin-related protein P-loop
E,195.365/Domain: kinesin motor domain homology <KMOT>
E,197.365/Domain: kinesin motor domain homology of (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSPFEKLAQSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 140; DB 1; Length 1056; ilarity 21.7%; Pred. No. 1.5; Conservative 56; Mismatches 100; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match B.1%; Score 140; DB 2; Local Similarity 25.0%; Pred. No. 1.6; hes 58; Conservative 35; Mismatches 95.
                                              R;Whitehead, C.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00839
A;Accession: Gull57
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: smc
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DSAQPQDENQSDA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 LHSKLDRKKAVDOHNAEA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  est Local
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

δλ

7;

us-09-673-763-8.rpr

Putative sensory t Human ORFX ORF1934

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

otal number Inimum DB s Maximum DB s

Searched:

Database :

```
Male-enhanced anti-
Mouse male enhance
Drosophila melanog
Novel human diagno
Putative P. abyasi
H. pylori secreted
H. pylori secreted
H. mylori secreted
Human mitosin. Ho
Human mitosin. Ho
Human mitosin. Ho
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanog
Staphylococcus aur
Staphylococcus aur
Novel human diagno
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Novel human diagno
Novel human diagno
Novel human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel bacterial infection specific proteins for treating and diagnosing chlamydial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia psittaci infection-specific protein IncA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IncA; infection; vaccine; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                         AAB96493
AAM42170
AAW4391
ABB68543
ABG21233
AAB621233
AAW20404
AAW20901
AAW20901
AAW23996
AAW339234
AAG39233
AAG39233
AAG39233
AAG39233
AAG39233
AAG36713
AAG36713
                                                                                                                                                                                                                                                                                                                                                                                                                    AAG36712
ABG13880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG05140
AAG48640
AAG48639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU33733
AAU36532
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB62371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY32173 standard; Protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0082438.
98US-0082588.
98US-0086450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US08744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
       10057
10057
13255
13255
13255
13255
13255
2866
2866
2866
2866
2867
1003
1103
1103
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11184
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bannantine JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYOR-) UNIV OREGON STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-633904/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia psittaci
                                                                           C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AA234587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1998;
21-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9953948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1999;
 140
140
139.5
138.5
136
136
136
136
137
133.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1999
                                                                                                                                                                                                                                                                                   130.5
130.5
130.5
130.5
130.5
130.5
130.5
130.5
130.5
130.5
129.5
129.5
129.5
129.5
129.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rockey DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32173
   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002, 09:21:19 ; Search time 53.52 Seconds (Without alignments) 736.756 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
5. /SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:*
6. /SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:*
7. /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
8. /SIDSI/gcgdata/hold-geneseqy-embl/AA1986.DAT:*
9. /SIDSI/gcgdata/hold-geneseqy-embl/AA1988.DAT:*
11: /SIDSI/gcgdata/hold-geneseqy-embl/AA1988.DAT:*
12: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
13: /SIDSI/gcgdata/hold-geneseqy-embl/AA1989.DAT:*
14: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
15: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
17: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
20: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
22: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia psittaci
Chlamydia pneumoni
Chlamydia trachoma
Human protein sequ
Drosophila melanog
Drosophila melanog
Human ORFX ORF3123
Human protein kina
Nucloalar/enfosoma
Human ORFX ORF2116
Human ORFX ORF2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      1733
1 MTVSTDNTSPVISRASSPTF ......DDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY34783
AAY32176
AAB95546
ABB611144
ABB611173
AAB43359
AAW02558
AAB42352
AAB42352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY32173
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                      US-09-673-763-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
22
22
22
22
22
22
22
22
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                               August 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612
1690
1690
1286
2053
1411
434
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0
```

1733 200 162.5 149 145 143.5 143.5 143.5 143.5

52 7 10 110 110

Score

Result Š us-09-673-763-8.rag

```
Griffais R;
                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                  Οý
                                                                                                                                                                                                                                                                                                                                                    g
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                      TNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                         LLQRICYLVKIIAAIALFVVGIAALVCLYLGSVISTPSLILMLAIMLVSFVIVITAIRDG 120
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                      1 MTVSTDNTSPVISRASSPIFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSP 60
                                                                                                                                                                                                                         9
                This sequence represents novel infection-specific protein IncA of Chlamydda psittaci strain GPIC. IncA is found in the inclusion membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than with the refractile elementary body form. The invention includes: a vaccine directed against the reticulate body form of Chlamydia comprising 1 or more infection-specific proteins (see AAX32170-78), including neathods for detection of infection-specific antibodies or antigens in a biological specime, and a method of using therapeutic agents specifically directed against infection-specific peptides, or the genes that code for such peptides, to treat chlamydial infection.
                                                                                                                                                                                                                TPSQVVRHMKQQ1QQFGEENTRLHTAVENLKAVNVELSEQ1NQLKQLHTRLSDFGDRLEA
                                                                                                                                                                                                                                                                                                                  NTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELR
                                                                                                                                                                                                                                                                                                                                                                LLKDSTINLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                   Length 355;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                   Score 1733; DB 20;
Pred. No. 4.4e-133;
                                                                                                                                                                                     Mismatches
    Claim 5; Page 39-40; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34783 standard; Protein; 397
                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; neutralising epitope
                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-IB01890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107078
97FR-0014673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae
                                                                                                                                                                                 Similarity
                                                                                                                                             355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998
                                                                                                                                                                                          355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY34783
                                                                                                                                               Sequence
                                                                                                                                                                         uery Match
                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                              ULT
(34783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                            δý
                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                       οy
```

```
13;
                                                                                                                                          AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and disease, sand is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584.75859) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 LREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sggeerrlreevsrftsengrltvitttletevkdlkaakdgltleieafrnengnlktt 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sspvnntpsapn-----kprssfiekvl- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSPVISRASSPTFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----qalkvllgqewvqeaqthvkamqeqiqalqaeilgmhnqstalqksvenllvqdq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      altrvvgellesenkisgacsalrgeieklaghetslggridamlagegni-----a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKIIAAIALFVVGIAALVCLYLGSVIS-----TPSL-ILMLAIMLVSFVIVITAIRDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ivakyilfai---aatsgalgtilglsgaltpgigiallviffvsmvllglilkdsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 aedleeqvsklseglealeringliganagdageisselkklisgwdskvvegintsi--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TENKTVIEQLKADAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 -VELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKS-VGTKVETMLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 200; DB 20; Length 397; 23.0%; Pred, No. 4.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis infection-specific protein IncA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 PSQVVRHMKQQIQQFGEEN-----TRLHTAVENLKAVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 FEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IncA; infection; vaccine; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Mismatches
                                                                                                     Page 760-761; Disclosure; 1912pp; English.
                                                     Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32176 standard; Protein; 273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 ESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             egvtalekmkqeaqkaese 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.
WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09953948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325
```

```
Novel bacterial infection specific proteins for treating and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents novel infection-specific protein Inch of Chlamydia trachomatis LGV-434 (serotype L2). Inch is found in the wich the membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than vaccine directed seanentary body form. The invention includes: a comprising or more infection specific proteins (see AAY32170-78), a vaccine, methods for detection of infection specific antibodies or antigens in a biological specimen; and a method of using such the verget of the vegetal specific antibodies the retrieval or method of using such the vegetal specifically directed against infection specific antibodies therefore the vegetal specific and vegetal veget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 filapqitivilalfitsla-----gnalylqktanlhlyqdlqr-----ev 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 IIPISIEAPISSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 vippsppapsysanrv-----pqpslmdkikkiaalasliligtigflallghlvg 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 sildeyknsteemrklfsgeiladlkgsvaslreeirfltplaeevrrlahngesltaai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 TENKTVIEQLKAD----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.4%; Score 162.5; DB 20; Length 2
21.4%; Pred. No. 3.2e-05;
tive 61; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:18167.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 45-46; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95546 standard; Protein; 612
                                                         99WO-US08744
                                                                                                                              98US-0082588.
98US-0086450.
                                                                                                      98US-0082438
                                                                                                                                                                                                                                               Rockey DD, Bannantine JP;
                                                                                                                                                                                             (UYOR-) UNIV OREGON STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                         WPI; 1999-633904/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 AA;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ34590
                                                 20-APR-1999;
                                                                                                 20-APR-1998;
                                                                                                                         21-APR-1998;
22-MAY-1998;
  28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95546
ID AAB9.
XX
AC AAB9
XX
DT 26-JT
XX
XX
KW Huma
8$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

8

```
The present invention describes primer sets for synthesising 5602

cull-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligordT primer and an oligonucleotide complementary

cull of the complementary strand of a polynucleotide which comprises one of

coligonucleotide comprisions at least 15 nucleotides in the specification, where the

coligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

conjouncleotide which comprises a 1'-end sequence. Where the

coligonucleotide comprises at least 15 nucleotides and the combination of

the 5'-end sequence/1'-end sequence is selected from those defined in

in gene therapy. The primers are useful for synthesiating polynucleotides,

coligonucleotide comprises a the set is calcuted from those defined in

coligonucleotide comprises a the set is selected from those defined in

coligonucleotide comprises a primers are also useful for the

coligonucleotide comprises a primers are also useful for the

coligonucleotide comprises and the primers are also useful for the

coliforularly full-length cDNAs. The primers are also useful for the

collection and/or diagnosis of the abnormality of the proteins encoded by

collection and/or diagnosis of the abnormality of the proteins encoded by

collection and and primers are useful for synthesistal and

collection and/or diagnosis of the abnormality of the proteins encoded by

collection and and protein and collection and also and and also and and also and and also and als
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Salto K, Ya
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.6%; Score 149; DB 22; I
3.5%; Pred. No. 0.0012;
Ve 47; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 18167; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                 99JP-0300253.
                                                                                                                                                                                                                                                                    11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                            99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                              Isogaí T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 AA;
                          Homo sapiens,
                                                                     EP1074617-A2.
                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                                                                                    7-AUG-1999;
                                                                                                                    07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

10;

Gaps

60;

Indels

Length 612;

23.5%;

Similarity

Local Best Loca Matches

Conservative

99

g ò

ò g ò 8 à

114 ITAIRDGTPSQVVRH---MKQQIQQFGEENTRLHTAVENLKAVNVEL-----SEQINQ 163

70 italkgalkeevsshdgemdklkegydaelgalresvee-atknvevlasrsntsegdga 128

164 LKQLHTR-LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKE

277 RKQELEEACSTLSHSIATLQE-----STTL---

=

303

----LK

a δλ

us-09-673-763-8.rag

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher entraryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57373-ABB72072).

(ABB57373-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SEQINQLKQL 167
1177 lkethlqlderqkkfeeleeklkqaqqseqklqqesqtskeklteiqqslqelqdsvkqk 1236
                                                      ---QLKADAQ-LREEQVRFLEKRKQE--LEEAC
                                                                                                      286 STLSHSIATLQESTTLLKDSTTNLH----AVESRLIGVMVQDGAESSTVEE----ASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 10311; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 10311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 145; DB 22;
20.6%; Pred. No. 0.011;
iive 57; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ENLKAVNVEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers
                                                                                                                                                                                                                                                                                                    ABB61173 standard; Protein; 1690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 VRHMKQQIQQFGEENTRLHTAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                             RTNLNALKELITENKTVIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
                                                                                                                                                                                                                       1357 enegnlages 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                    336 DDSAQPQDEN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABL05276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local $
                                                                                                                                                                                                                                                                                                                                            ABB61173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                               ABB61173
                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                         g
                                                                                                                                                                                            Óλ
                                                                                                                                                                                                                         g
                                                                                    g
                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               įs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABB57737-ABB12072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and in elucidating cell signalling and in signation in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL01840 ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1057 iknlqeevtkaktenlelstgtqttikdlqerleitnaelqhkekmasedaqkiadlktl 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TFSQEAVQAMMSSVTEL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SEQINQLKQL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                       245 lknemenerwhlgktieklgkemadiveasrtstlelqngldeykeknrrelaemgrglk 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :-
-
:-
-
:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 10224; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 145; DB 22; Length 1690;
Pred. No. 0.011;
7; Mismatches 99; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HTRLSDFGDRLEANTGDFTALIADFQLSL---
                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 10224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 VRHMKQQIQQFGEENTRLHTAV-----ENLKAVNVEL---
                                                                                     DSTINLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 FKSVGTKVETMLSPFEKLAQSLKE----
                                                                                                                                                                                      ABB61144 standard; Protein; 1690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::
::
::
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%;
nilarity 20.6%;
Conservative 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL05247
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                               ABB61144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                         304
                                                                                                          305
                                                                                                                                                                               ABB6114
                                                                                                                                                             RESULT
```

10;

Gaps

g

Óλ

g δy

δ

8888888**%**8

```
*8888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whuman; open reading frame; ORFX; detection; cytostatic; hepatotropic; W vulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective; W anticonvulsant; oateopathic; antiarthritic; immunosuppressant; cardiant; M munostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; w intibacterial; immunosuppressive; antidiabetic; w antiviral; antibacterial; antifungal; antirheumatic; antithyroid; w antiviral; antibacterial; antifungal; actirheumatic; antithyroid; w antianaemic; gene therapy; cancer; proliferative disorder; hypertension; w neurodegenerative disorder; osteoarthritis; graft vs host disease; chaletes mellitus; hypothyroidism; SCID; Albs; severe combined immunodeficiency; maleraria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; w thrombosis; contraceptive.
1057 ikniqeevtkaktenlelstgtqttikdiqerleitnaelqhkekmasedaqkiadiktl 1116
                                         1117 vealqvananisatnaelstvlevigaeksetnhifelfemeadmnserliekvtgikee 1176
                                                                               199 FKSVGTKVETMLSPFEKLAQSLKE-------TFSQEAVQAMMSSVTEL 239
                                                                                                         RINLNALKELITENKTVIE------QLKADAQ-LREEQVRFLEKRKQE--LEEAC 285
                                                                                                                                                            335
                        ------HTRLSDFGDRLEANTGDFTALIADFQLSL--------EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, prolliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                  286 STLSHSIATLQESTTLLKDSTTNLH----AVESRLIGVMVQDGAESSTVEE----ASQ
                                                                                                                                                                                                                                                                                                                                     Human ORFX ORF3123 polypeptide sequence SEQ ID NO:6246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 5433-5436; 5507pp; English.
                                                                                                                                                                                                                                                                     AAB43359 standard; Protein; 1286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127607
                                                                                                                                                                                                                                                                                                              08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
                                                                                                                                                                                                           :: | |:
1357 enegnlqges 1366
                                                                                                                                                                                            DDSAQPQDEN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57.
N-PSDB; AAC77568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-0CT-2000
                                                                                                                                                                                                                                                                                            AAB43359;
                      168
                                                                                                                                                                                            336
                                                                                                                                                                                                                                                           AAB43359
                                                                                                                                                                                                                                                  RESULT
 a
                      à
                                        q
                                                              ò
                                                                                 g
                                                                                                                        g
                                                                                                       ò
                                                                                                                                                                    g
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                           ö
```

```
AX AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activitites such as: cytostatic; hepatotropic; vulnerary; cosquences have activitities such as: cytostatic; hepatotropic; vulnerary; antipsorialic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; cosquences; mannosuppressant; munosuppressant; antidiabetic; hypotensive; dermatological; immunosuppressant; antidiabetic; hypotensive; dermatological; immunosuppressive; antithyroid; and antibarcerial; antivingal; antirheumatic; the presence of or predisposition to, or preventing or treating continued associated with an ORFX-associated disorder. The presence of or predisposition to, or preventing or treating cucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, cucleic acids and nucleic acids may be used to treat cancers, cortors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthitis, cortain the second of the proteins and nucleic acids may be used to treat cancers, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus cortains of fungal infection, malaria, autolimune disorders, asthma, allergies, aplastic ansemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 DFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFE-KLAQS---LKETF--SQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, protein kinase, PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 RHMKQQ---IQQFGEENTRLHTAVENLKAVNVELSEQI-----NQLKQLHTRLS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 rnmkaqeemiselrqqkfyletqagkleaqnrkleeqlekishqdhsdknrlleletrlr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 -----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVQAMMSSVTELRTNLNALKE---LITENKTVIEQLKAD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%; Score 143.5; DB 21; Length 24.3%; Pred. No. 0.0099; tive 47; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU03501 standard; Protein; 2053 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2000; 2000WO-US32085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0167482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein kinase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200138503-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU03501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU03501
```

(SUGE-) SUGEN INC.

```
AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides or serine/threonine kinase (PTK and STK) families. The polynucleotides corrected in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular cancers (especially cancers of haematopoletic origin), cardiovascular cancers (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), commune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. asthma), infectious cancers (e.g. HIV) and reproductive disorders (e.g. infertility).

Compared therapy and as DNA probes in diagnostic assays.

Compared therapy and as DNA probes in diagnostic assays.

Compared therapy and as DNA probes in diagnostic assays.

Compared therapy and as DNA probes and in assays to identify medulators of protein kinase expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                           ...yuwsing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :||: : |:: :||: :||: eeigaltahrdeigrkfdalrnsctvitdleeglngltednaelnngnfylskgldeasg 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NQLKQLHTRLS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 -----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 DFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFE-KLAQS----LKETF--SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evsleheegklelkrgitelgisigeresgltalgaaraalesgirgakteleettaeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatic disease; antigen; diagnosis;
         Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 EAVQAMMSSVTELRTNLNALKE---LITENKTVIEQLKAD---
         Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.3%; Score 143.5; DB
ilarity 24.3%; Pred. No. 0.019;
Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 RHMKQQ---IQQFGEENTRLHTAVENLKAVNVELSEQI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleolar/endosomal auto-antigen p162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW02258 standard; Protein; 1411 AA
         Manning G,
                                                                                                                                                                            Claim 7; Figure 2; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Auto-antibody; p162;
            Whyte D,
Clary D;
                                                               WPI: 2001-343950/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2053 AA;
                                                                                 N-PSDB; AAS06701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19515514-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1996.
              Plowman GD,
Flanagan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW02258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρp
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
```

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antiened; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 LE-KRKQELEEACSTLS---HSIATLQ----ESTTLLKDSTTNLHAVESRLIGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LRTNLNALKELITENKTVIEQLKADAQLREEQVRF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 MKQQIQQFGEE-----NTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transformed cells can be cultured to produce the antigen p162, for in exact (differential) diagnosis of rheumatic disease, i.e. they can detect, in immunoassays, Western blots, etc., rheumatism-specific auto-antibodies. The antigen can be used therapeutically, in the removal of auto-antibodies from the circulation, or when coupled to a cytotoxin, the elimination of auto-antibody-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :| | | : :| | : ::| | :::| | :::
872 sksefekengkgkaaildlektckelkhqlqvqmentlkegkelkkslekekeashqlkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding nucleolar-endosomal auto-antigen - useful for exact diagnosis of rheumatic disease, in gene therapy and for removal of specific auto-antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 NTGDF-----TALIADFQLSLEEFK-SVGTKVETMLSPFEKLAQSL-KETFSQEAVQA
                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF2116 polypeptide sequence SEQ ID NO:4232.
                                                               (PRIV-) PRIVATES INST IMMUNOLOGIE & MOLEKULARGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESSTVEE---ASQDD--SAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB42352 standard; Protein; 434 AA.
                                                                                                                                                                                                                                    Claim 1; Fig 2; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
         95DE-1015514
                                     95DE-1015514
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 24.03
                                                                                                                                                                                                                                                                                                                                                             producing lymphocytes.
                                                                                                                           WPI; 1996-403153/41.
N-PSDB; AAT58751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 MMSSVTE-----
                                                                                                                                                                                                                                                                                                                                                                                          1411 AA;
                                                                                                  Seelig HP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001
         27-APR-1995;
                                      27-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB42352;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                    Renz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
```

us-09-673-763-8.rag

```
AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORRX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; cartipsoriatic; antiparkinsonian; noticopic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; contidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirhemmatic; the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used for determining pathological conditions associated with an ORFX-associated disorder. The vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allegies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VRHMKOQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSD--FGDRLEANTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENKTV---IEQLKADAQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aldenakitqqiee----eriq-hqqkvkeleeqi------enetlhkeihnikqqle 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 iKelrdqivsyqeekilaielenlksklvevieevnkvkqektvlnsevlegrkvlekc 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.1%; Score 140.5; DB 21;
26.4%; Pred. No. 0.0038;
tive 32; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 3424-3425; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 DFTALIA-----DFQLSLEEFKSVGTKVETMLS----
                                                                                                                                                                                                                                                   99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                             31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                  30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                              Leach M;
                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAC76561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 434 AA;
                                                                                                                                           WO200058473-A2.
                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                   31-MAR-1999;
                                                                                                                                                                                                                                                                    02-APR-1999;
05-APR-1999;
                                                                                                                                                                             05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
SXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
```

```
This sequence represents the human kinesin, KSP-S553, which may be used in the method of the invention to screen for drug candidates and bloactive agents. The method comprises combining the candidate of the candidate or the bloactivity of KSP, and determining the effect in the bloactivity of KSP may be determined by assays for determining changes in the mitotic spindle, particularly inhibition of mitosis, to determine the effect of candidate agents on apoptosis and necrosis. The method of the invention is useful for screening for drug assays The method of the invention is useful for screening for drug candidates (especially bloactive agents and proteins) which effect the bloactivity of KSP, and/or expression of KSP, where the cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for drug candidates and treating cancer by using kinesin KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 VITAIRDGTP-----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 vitalvertphvpyreskitrilgdslg--grtrtsl---latispaslnleetistley 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSPFEKLAQSLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 ah-raknilnkpevngkitkkalikeyteeierikrdlaaarekngvyiseenfrvmsgk
                                                                                                                                                                                                        Human; kinesin; KSP; drug screening; mitotic spindle; mitosis;
ATP hydrolysis; apoptosis; necrosis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                 Sakowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 140; DB 22;
21.7%; Pred. No. 0.0062;
.1ve 56; Mismatches 100;
 LREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDS
                                                                                                                                                                                                                                                                                                                                                                                                                             Mak J,
                                                                                             AAB47215 standard; Protein; 575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 8; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Beraud C,
                                                                                                                                                                                                                                                                                                                                     26-OCT-2000; 2000WO-US29570.
                                                                                                                                                                                                                                                                                                                                                                   99US-0428156.
                                                                                                                                                   18-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            (CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Wood KW, Finer JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-300550/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC85783
                                                                                                                                                                               Human KSP-S553
                                                                                                                                                                                                                                                                                WO200131335-A2.
                                                                                                                                                                                                                                                                                                                                                                27-OCT-1999;
                                                                                                                                                                                                                                                                                                          03-MAY-2001.
                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                           AAB47215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
                                                                                                           g
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

10;

```
This sequence represents the human kinesin, KSP, which may be used in the method of the invention to screen for drug candidates and bloactive agents. The method comprises combining the candidate and a cell expressing recombinant KSP, and determining the effect of the candidate on the bloactivity of recombinant KSP. Changes in the bloactivity of KSP may be determined by assays for determining and ATP hydrolysis. It may also be determined by performing assays and ATP hydrolysis. It may also be determined by performing assays to determine the effect of candidate agents on apoptosis and necrosis. The method of the invention is useful for screening for drug candidates. The method of the invention is useful for screening for drug candidates (especially bloactive agents and proteins) which effect the bloactivity of KSP binding to KSP and/or expression of KSP, where the cells are
                                                                                                                             282 EEACSTLSHSIATLQES--TTLLKDSTINLHAVESRLIGVMVQDGAESSTVEEASQD--- 336
                                                                                                                                               ah-raknilnkpevnqkltkkalikeyteeierlkrdlaaarekngvyiseenfrvmsgk 411
167 LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSPFEKLAQSLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for drug candidates and treating cancer by using kinesin
                                                                                222 ETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Kinesin; KSP; drug screening; mitotic spindle; mitosis; ATP hydrolysis; apoptosis; necrosis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 140; DB 22; Length 1
21.7%; Pred. No. 0.015;
tive 56; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mak J,
                                                                                                                                                                                                                                                                                                                   AAB47212 standard; Protein; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beraud C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000; 2000WO-US29570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0428156.
                                                                                                                                                                                                         337 ----DSAQPQDENQSDA 349
                                                                                                                                                                                                                                     513 lhskldrkkavdqhnaea 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood KW, Finer JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-300550/31.
N-PSDB; AAC85780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200131335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Human KSP
                                                                                                                                                                                                                                                                                                                                                        AAB47212;
                                                353
                                                                                                                                                                                                                                                                                              RESULT 1
AAB47212
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                 ŏλ
                                                                                                                                                                              Dp
                                                                                                                                                                                                                ò
                                                                                                               g
                                                                                QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a bimc homologue, designated Eg5. BimC is a kinesin related protein, which is essential for fungal viability. Is a kinesin related protein, which is essential for fungal viability. The specification describes a method of identifying modulators of bimc. The method comprises adding a test agent to a mixture comprising bimc. Or protein that directly or indirectly produces ADP or phosphate, subjecting the mixture to an enzymatic reaction that uses the ADP or phosphate. Or and determining the enzymatic activity in presence and absence of test compound. A change in the activity level between the presence of test of the candidate agent indicates a modulator of the target protein of the method is useful for identifying a modulator, e.g. cuntifungal agents, of bimc. The modulators can be used, for example, to inhibit the growth or spread of fungi, mould, fruit flies, etc.. The inhibit the growth or spread of fungi, mould, fruit flies, etc.. The condulators can be used for preventing and treating infections caused computations. Ascomycetes, plasmodiophoromycetes, open comycetes, Zygomycetes, and Basidlomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a modulator, e.g. antifungal agent, of a target protein comprising bimc or its fragment by determining enzymatic activity of a reaction, in the presence and absence of the compound, that uses ADP or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 VITAIRDGTP----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEACSTLSHSIATLQES--TTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD--- 336
                                         bimC; kinesin related protein; fungal viability; antifungal; Eg5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 21.7%; Pred. No. 0.015; 56; Conservative 56; Mismatches 100;
                                                                                                                                                                                                                                                                                                       Amino acid sequence of bimC homologue, Eg5.
                                                                                                                                                                                                          AAG67419 standard; Protein; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beraud C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2000; 2000US-0541782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2000; 2000US-0541782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphate produced by bimC
                                                                                                                   | ; |:: ::|
513 lhskldrkkavdqhnaea 530
                                                                                                 349
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CYTO-) CYTOKINETICS INC.
                                                                                                 337 ----DSAQPQDENQSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-540724/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1057 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH78013
                                                                                                                                                                                                                                                                                                                                                                 fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                US6284480-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2001.
                                                                                                                                                                                                                                                                                13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nislow CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                    AAG67419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8×3333333333333×3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                    2×2×5×
                                                                       a
                                                                                                        δŏ
                                         οy
```

KSP

ж

10;

Gaps

46;

Length 1057;

```
Putative sensory transduction histidine kinase and response regulator #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to
113 VITAIRDGIP----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166
                          298 vitalvertphvpyreskltrilgdslg--grtrtsi---latispasinleetlstley 352
                                                      LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSFFEKLAQSLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                         353 ah-raknilnkpevngkltkkalikeyteeierlkrdlaaarekngvyiseenfrvmsgk
                                                                                                         ETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL
                                                                                                                            282 EEACSTLSHSIATLQES--TTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD---
                                                                                                                                                                               New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lecompte 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thierry JC, Prieur D, Dietrich J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Pages 1203-1205; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                              AAB96493 standard; Protein; 739 AA.
                                                                                                                                                                                                                  337 ----DSAQPQDENQSDA 349
                                                                                                                                                                                                                                           513 lhskldrkkavdghnaea 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99FR-0005034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99FR-0005034
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forterre P, 1
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                    29-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2792651-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-0CT-2000.
                                                                                                                                                                                                                                                                                                                                           AAB96493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                          222
                                                                           셤
                                                    ò
                                                                                                         à
                                                                                                                               qq
                                                                                                                                                       ò
                                                                                                                                                                                      a
                                                                                                                                                                                                                  ò
```

```
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunositimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; antiviral; antiviral; antidiabetic; antiviral; antiviral; antidiabetic; antiviral; antidiabetic; antiviral; antidiamatory; ancidancemic; que therapy; cancer; proliferative disorder; hypertension; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosic; cartilage damage; antiinflammatory disease; coaquiation;
IIAAIAL-FVVGIAALVCLY-LGSVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVRH 128
                  185 FTALLADFQLSLEEFK-SVGTKVETMLSPFEKLAQSLKETFSQ--EAVQAMMSSVTELRT 241
                                                                                                                              --TLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDG--AESSTVEEASQDDSAQ 340
                                                                                                                                                                                                                                        531 iediqhmmsrieetvskvaemsrnleeitnvitslaeqtnllalnaaleaarageagr 588
                                                                      129 MKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANT----GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                  242 NLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACS-----
                                                                                                                                                                                                                                                                                                                                                                                                       Human ORFX ORF1934 polypeptide sequence SEQ ID NO:3868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 3015-3016; 5507pp; English.
                                                                                                                                                                                                                                                                                                                     AAB42170 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602362/57.
N-PSDB; AAC76379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                   AAB42170;
                                                                                                                                                                                                                         287
                                                                                                                                                                                                                                                                                                            AAB42170
                        g
                                                    à
                                                                           엄
                                                                                                          ò
                                                                                                                                     g
                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                g
```

13;

Gaps

45;

Length 739;

Ouery Match 8.0%; Score 139.5; DB 22; Length Best Local Similarity 21.1%; Pred. No. 0.0096; Matches 63; Conservative 66; Mismatches 124; Indels

```
C which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX acquences have activities such as: cytostatic; hepatotropic; vulnerary: consteopathic; anticonvulsant; antiarthritic; immunosuppressant; contidiabetic; anticonvulsant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antidiabetic; hypotensive; dermatological; antiformedical; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating culling associated with an ORFX-associated disorder. pathological conditions associated with an ORFX-associated cancers, contilions associated with an ORFX-associated concerts, or preventing or treating culling and nucleic acids may be used to treat cancers, proliferative disorders, eurodegenerative disorders, osteoarthritis, crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, allergies, aplastic anaemia, burns, and contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 RKQELEEACSTLSHSIATLQ-ESTTLLKDSTTNLHAVESRL------IGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 LKQLHTR-LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 gtemrvkliqeenekiqgrseelerrvaqlqrqiedlkgdeakaketikkyegeirqlee 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 TF-----SQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 alvharkeekeavsarraleneleaaggnlsqttqeqkqlseklkeeseqkeq----lrr 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 lknemenerwhigktiekiqkemadiveasrtstlelqnqldeykeknrrelaemqrqlk 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ITAIRDGTPSQVVRH----MKQQIQQFGEENTRLHTAVENLKAVNVEL-----SEQINQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.0%; Score 138.5; DB 21; Length
Best Local Similarity 22.8%; Pred. No. 0.004;
Matches 59; Conservative 52; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 ESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                           888888888888888888888
```

Search completed: August 13, 2002, 09:23:46 Job time: 147 sec

~

us-09-673-763-8.rsp

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

protein search, using sw model • OM protein

August 13, 2002, 09:24:24 ; Search time 17.41 Seconds (without alignments) 789.514 Million cell updates/sec Run on:

US-09-673-763-8 1733 1 MTVSTDNTSPVISRASSPIF......DDSAQPQDENQSDAGEHKDS 355 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

himum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	014578 homo sapien P32380 saccharomyc P5273 homo sapien P06198 schlastosoma P47460 mycoplasma P49025 mus musculu P1055 homo sapien P12597 mus musculu P25386 saccharomyc O9v623 homo sapien P2538 haloarcula P39922 hydra atten O10411 schlzosacch P13692 enterococcus P62209 mus musculu P62494 homo sapien P1284 caenorhabdi P1284 caenorhabdi P1284 caenorhabdi P1284 caenorhabdi P1284 homo sapien P35749 homo sapien P21282 homo sapien P21282 homo sapien P21282 homo sapien P21282 homo sapien P21249 onchocerca P21249 onchocerca P21249 onchocerca P21270 homo sapien O908538 mus musculu O91100 rattus norve P02562 oryctolagus
SUMMARIES	MAN ASA AN AN AN CGE USE USE USE WAN AN AN AN AN AN AN AN AN AN AN AN AN A
SUMM	CTRO. HUMAN NUF1_YEAST BGS_HUMAN MYSP_SCHMA HMW2_MYCGE CTO_MOUSE MYH3_HUMAN MYH8_HUMAN HTR2_HALVA WYR3_HYDAT WS01_YEAST WS01_YEAST WS01_YEAST WYR3_HYDAT WS01_YEAST WYR3_HYDAT WS01_YEAST WYR3_HYDAT WS01_YEAST WYR3_HYDAT WYR3_HYDAT WYR3_HYDAT WYR4_HUMAN WYR4_RABIT MYH1_HUMAN WYCEBACSU CENE_HUMAN WYCH_HUMAN WYH1_HUMAN WYCH_HUMAN WYCH_HUMAN WYH1_HUMAN
DB	
% Query Match Length	1286 1986 1986 1980 1180 1180 1180 1180 1180 1180 1180
8 Query Match	88888677777777777777777777777777777777
Score	
Result No.	11008976897789778978897888788878887888788878

InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR000861; REM_repeat.
Pfam; PP00780; CMH; 1.
Pfam; PP00130; DAG_PE-bind; 1.
SMART; SM00109; CI; 1.
SMART; SM00213; PH; 1.

InterPro; IPR001180; CNH. InterPro; IPR002219; DAG_PE-bind.

Q11102 caenorhabd1 P35748 oryctolagus P10587 gallus gall Q05870 schistosoma P58301 pyrococcus Q09591 caenorhabd1 Q42184 gallus gall P3580 homo sapien P54697 dictyostella P17120 emericella P02566 caenorhabd1 P93203 lycopersico
YL17_CABEL MYHB_RABIT MYHB_CHICK MYSP_SCHJA RN50_PYEFU MIX1_CABEL MIX1_CABEL MYHA_HUMAN MYSJ_DICCI BINC_EMENI MYSB_CAEEL MYSB_CAEEL
нанананана
1130 1972 1978 866 882 1244 11434 11976 1184 1966
77777777777777777777777777777777777777
126.5 126.5 126.5 126 126 126 126 126 126 125 125.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A MEDLINE-99246063; PubMed-10231032;

RA Magase T., Ishikawa K. I., Suyama M., Kikuno R., Hirosawa M.,

RA Magase T., Ishikawa K. I., Suyama M., Kikuno R., Hirosawa M.,

RA Mayajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT Tediction of the coding sequences of unidentified human genes. XIII.

RT The complete sequences of 100 new cDNA clones from brain which code

RT The complete sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new cDNA clones from brain which code

RT The Complete Sequences of 100 new code in the Co
                                                                                                                                                                                                                                                                                        Homo saplens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                    CTRO_HUMAN STANDARD; PRT; 1286 AA. 014578; Q9UP27; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAR-2002 (Rel. 41, Last annotation update) Citron protein (Rho-interacting, serine/threonine kinase 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Connell M., Goela D., Harper M.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 347-1286 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC002563; AAB71327.1; -.
EMBL; AB023166; BAA76793.1; -.
MIM; 605629; -.
                                                                                                                                                                                                                                              (Fragment).
CIT OR STK21 OR KIAA0949.
      CTRO_HUMAN
RESULT
```

```
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                      Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                 Local Sim
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
EG5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID AC DIT OC OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mirzayan C., Copeland C.S., Snyder M.; "The NUF1 gene encodes an essential coiled-coil related protein that is a potential component of the yeast nucleoskeleton."; J. Cell Biol. 116:1319-1332(1992).
                                                                                                                                                                                                                                                                             173 DFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFE-KLAQS---LKETF--SQ 226
                                                                                                                                                                                                                                                                                            EEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG 253
                                                                                                                                                                                                                                                    74 RNWKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLELETRLR 133
                                                                                                                                                                                                                              ----NQLKQLHTRLS 172
                                                                                                                                                                                                                                                                                                                                                                          ----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLI 317
                                                                                                                                                                                                                                                                                                                                                                                         254 ANDEIVQLRSE-VDHLRREITEREMQLISOKQIMEALKTICIMLEEQVMDLEALNDELL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kilmartin J.V., Dyos S.L., Kershaw D., Finch J.T.,
"A spacer protein in the Saccharomyces cerevisiae spindle poly body
whose transcript is cell cycle-regulated.";
J. Cell Biol. 123:1175-1184(1993).
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            EAVQAMMSSVTELRTNLNALKE---LITENKTVIEQLKAD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-ocr-1993 (Rel. 27, Created)
01-ocr-1993 (Rel. 27, Last sequence update)
01-ocr-2001 (Rel. 40, Last annotation update)
16-ocr-2001 (Rel. 40, Last annotation update)
NUF1 protein (Spindle poly body spacer protein SPC110).
NUF1 OR SPC110 OR YDR356W OR D9476 3.
Saccharowyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Rucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Langston Y., Latreille P., Le T., Johnston D., Johnston D., Johnston L., Andrews S., Miller N., Nhan M., Pauley A., Peluso D., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
                                                                                                                                                                                                         49;
                                                                                                                                                                                   Length 1286;
                                                                                                 PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                          Indels
                                                                                                                                    SH3-BINDING (POTENTIAL).
W; 498101F79EA75E85 CRC64;
                                                               COILED COIL (POTENTIAL). RHO/RAC BINDING.
                                                                                                                                                                                     DB 1;
                                         binding; SH3-binding
                                                                                                                                                                                    Score 143.5; Di
Pred. No. 0.47;
                                                                                                                                                                                                                                    127 RHMKQQ----IQQFGEENTRLHTAVENLKAVNVELSEQI-
                                                                                                                                                                                                            47; Mismatches
     DAG_PE_BIND_DOM_1; 1.
DAG_PE_BIND_DOM_2; 1.
PH_DOMAIN; 1.
                                                                                        POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=94064779; PubMed=7503995; MEDLINE=94064779; PubMed=7503995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92176232; PubMed=1541631;
                                                                                                                                                     ¥Σ
                                                                                                                                                                                      8.3%;
                                                                                                                                                  146506
                                          coil; Phorbol-ester
                                                                                                                                                                                                                Conservative
                                                                                                                                                     AA;
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
         PS00479;
PS50081;
                                PROSITE; PS50003;
                                                                    <1
365
509
622
702
851
1212
                                                                                                                                                                                                                58;
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                        Query Match
Best Local
                                                        NON_TER
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUFI_YEAST
                                              Coiled
                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE DE OS
                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                             g
```

```
8
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Kinesin-related motor protein E95 (Kinesin-like spindle protein HKSP)
(Thyroid receptor interacting protein 5) (TRIP5) (Kinesin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 LEANTGDFTALIADFQLSLEEFK-----SVGTKVETMLSPFEKLAQSLK----ETFSQ- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AVNVELSEQINQLKQLHTRLSDFGDR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAVQAMMSSVTELRTNLNALKELITENKTV-----IEQLKADAQLREEQVRFLE
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEOSKELETON. POTENTIAL
ROLE IN CROSSLINKING FILAMENTS OR ANCHORING OTHER MOLECULES. IT
IS ESSENTIAL FOR GROWTH.
-!- SUBCELLULAR LOCATION: NUCLEAR; TIGHTLY ASSOCIATED WITH THE
NUCLEUS, IT IS PRESENT IN A GRANULAR PATTERN THAT EXCLUDES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 MDLQLKQKQNESKRLKDELNELETKFSENGSQSSAKENELKMLKNKIAELEEEISTKNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 0.45; 56; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04FAA074BB8A0BC8 CRC64;
                                                                                                                                                                                                        NUCLEOLUS.
PIM: MAY BE REGULATED BY PHOSPHORYLATION EVENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 1;
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 MKQQIQQFGEENTRLHTAVENLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EG5_HUMAN STANDARD; 1
P52732; 015716;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequ
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 211582; CAA77668.1; --
EMBL; X73297; CAA51733.1; --
EMBL; US3872; AA864791.1; --
PIR; S26710; S26710.
PIR; S34288; S34288.
SGD; S0002764; NUF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 DDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 ENYEKQLESLRKDIEEXKES 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.18; 23.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
```

m

```
MYSP_SCHMA
P06198;
01-JAN-1988 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                              Paramyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen B
                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                               222
                                                   167
                                                ò
                                                                            g
                                                                                                          ò
                                                                                                                                        qq
                                                                                                                                                                         δ
                                                                                                                                                                                                    q
                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmil to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MOTOR PROPERIN REQUIRED FOR ESTABLISHING A BIPOLAR SPINDLE. BLOCKING OF EGS PREVENTS CENTROSCOME MIGRATION AND ARREST CELLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS.

1. SUBUNIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE PRESENCE OF THYROID HORMONE RECEPTOR IN THE PRESENCE OF THYROID HORMONE.

1. PTM: PHOSPHORYLATED EXCLUSIVELY ON SERINE DUBING S PHASE, BUT ON BOTH SERINE AND THR-927 DURING MITOSIS, SO CONTROLLING THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING
                            MEDLINE-90128120; PubMed-8548803; Blangy A., Lane H.A., D'Herin P., Harper M., Kress M., Nigg E.A.; Phosphorylation by p34cdc2 regulates spindle association of human Eg5, a kinesin-related motor essential for bipolar spindle formation
                                                                                                                                                                                                                                              NEDLINE-95295737; Pubmed-7776974; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; "Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                PHOSPHORYLATION SITE THR-927, AND MUTAGENESIS.
                                                                                                                                                     MEDLINE-98369052; PubMed-9701554; Whitehead C.M., Rattner J.B.; "Expanding the role of HsEg5 within the mitotic and post-mitotic phases of the cell cycle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00411, KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOT protein; Microtubules; ATP-binding; Coiled coil; Mitosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
PHOSPHORYLATION (BY CDC2).
T-AS: NO MITOTIC PHOSPHORYLATION.
BINDING TO SPINDLE APPARATUS.
RNS -> EL (IN REF. 2).
WW: E322F2141BEF1601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 0.59;
56; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 140;
21.7%; Pred. No. 0
                                                                                                                                                                                                                     Cell Sci. 111:2551-2561(1998).
                                                                                                                                                                                                                                                                                                                                             Endocrinol. 9:243-254(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X85137; CAA59449.1; -.
EMBL; U37426; AAA86132.1; -.
EMBL; L40372; AAC41739.1; -.
HSSP; P33176; 1BG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA; 119273
                                                                                                          83:1159-1169(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 21.7
nes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
480
764
1112
927
927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676
                  SEQUENCE FROM N.A.,
MEDLINE-96128120; Pu
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674
1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 148760;
                                                                                                                                                                                                                                                                                                                              receptor."
Mol. Endoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
8888888888888888888888888888888888
```

10;

Gaps

46;

:: --::

113 VITAIRDGTP----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166

= .. = =

ô

--

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                    512
298 VITALVERTPHVPYRESKLTRILQDSLG--GRTRTSI---IATISPASLNLEETLSTLEY 352
                                                            353 AH-RAKNILNKPEVNQKLTKKALIKEYTEEIERLKRDLAAAREKNGVYISEENFRVMSGK 411
                                                                                                    ETFSQEAVQAMMSSVTELRINLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKOEL 281
                                                                                                                                                                       282 EEACSTLSHSIATLQES--TTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD--- 336
                                  LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSPFEKLAQSLK 221
                                                                                                                                      412 LTVQEEQIVELIEKIGAVEEELNRVTELFMDNKNELDQCKSDLQNKTOELETTOKHLQET 471
                                                                                                                                                                                           SEQUENCE OF 303-742 FROM N.A.
MEDLINE-87018840; PubMed-3094144;
Land D.B., Pearce B.J., James S.L., Sher A.;
"Identification of paramyosin as schistosome antigen recognized by intradermally vaccinated mice.";
Science 234:593-596(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paramyosin is the Schistosoma mansoni (Trematoda) homologue of antigen B from Taenia solium (Cestoda)";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laclette J.P., Landa A., Arcos L., Willms K., Davis A.E., Shoemaker C.B.,
                                                                                                                                                                                                                                                                                                                                                                                               01-JNN-1988 (Rel. 06, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       866 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gen B from Taenia solium (Cestoda).";
Blochem. Parasitol. 44:287-296(1991).
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-91270282; PubMed-2052029;
                                                                                                                                                                                                                                         337 ---- DSAQPQDENQSDA 349
                                                                                                                                                                                                                                                                             513 LHSKLDRKKAVDQHNAEA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M14163; AAA29915.1; -.
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6183;
```

FT FT FT FT SO

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
W; 11D093AF173284FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03403; Seryl_LkNA_N; J:
Cytadherence; Structural protein; Coiled coil; Complete |
Cytadherence; Structural protein; Coiled Coil (POTENTIAL).
DOMAIN 914 1591 COILED COIL (POTENTIAL).
DOMAIN 1632 1723 COILED COIL (POTENTIAL).
COMBAN 1777 1804 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 139; DB Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
MEDLINE-96128238; PubMed=8543060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003364; Seryl_tRNA_N. Pfam; PF02403; Seryl_tRNA_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1805 AA; 216252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 33, Created) (Rel. 33, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.0%;
illarity 23.1%;
Conservative 44
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U39701; AAC71437.1; -. EMBL; U02165; AAD12447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1591
1723
1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 ENLOQEKO 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914
1632
1777
                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AQPQDENQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (
01-FEB-1996 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTRO MOUSE
P49025;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; MG218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
CTRO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {}^{Q}_{Y}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δŽ
SO THE TENT WAS DRAWNED BY THE TENT OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=ATCC 33530 / G-37;

STRAIN=ATCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;

Praser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Ruyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 TLQESTTLLKDSTTNLHAV---ESRL---IGVMVQDGAESSTVEEASQD-----DSAQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKS-TTRTIEELTVTITEMEVKYKSELSRLKKRYESNIADLEIQLDTANKANANLMKENK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Cytadherence high molecular weight protein 2 (Cytadherence accessory
                                                                                                                                                                                                                                                                                                                                                                                                        183 VNTLTSQNSQLESENLRLKSLVNDLTDKNNLLERENRQMNDQVKELKSSLRDANRRLTDL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FGDRLEANTGDFTALIAD------FQLSLEEFKSVGTKVETMLSPFEKLAQSL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LITENK 254
                                                                                                                                                                                                                                                                                                                                                                 VRHMKQQIQQFGEENTRLHTAVEN-----LKAVNVELSEQINQLK----QLHTRLSD- 173
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVIEQLK-----ADAQLREEQVRFLE----KRKQ---ELEEACSTL-----SHSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EALRSQLEAERDNLASALHDAEEALHDMDQKYQASQAALNHLKSEMEQRLRERDEELESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                         ; DB 1; Length 866; 0.53;
                                                                                                                                                                                                                                                                                                                    93; Indels
        2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 33530 / G-37;

MEDLINE=94075230; PubMed=8253680;

PETERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;

PARTICLE STREET AND STREET OF THE PROPRIET OF THE PROPR
     DQVKEL -> GSSQRI (IN REF. 2)

SS -> KL (IN REF. 2).

V -> L (IN REF. 2).

T -> I (IN REF. 2).

G -> E (IN REF. 2).

G -> E (IN REF. 2).

S -> E (IN REF. 2).

S -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KETFSQEAVQAMMSSVTEL----RINLNALKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1805 AA.
                                                                                                                                                                                                                                                                                                                          67; Mismatches
                                                                                                                                                                                                                                                                  Score 139;
                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE OF 557-659 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                  8.0%;
ilarity 21.4%;
Conservative 6
                 428
431
637
639
691
720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682 LADELROEQGNYK 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PODENQSDAGEHK
                    423
430
637
639
691
720
866 AA;
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMWZ OR MG218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMW2_MYCGE
                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 2)
                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMW2_MYCGE
                                                                                                                                                                                                                                                                              Query Matc}
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                Matches
```

8444B

qq δ

οy g QΥ Пр ò q

Dp

```
13;
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HWW PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS IN THE MYCOPLASMAL MEMBRANE AT THE ATTACHMENT ORGANELLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AIRDGTPSQVVRHMKQQIQQFGEENTRLHTAVE---NLK---AVNVELSEQINQLKQLHT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 EKRREIDTLLTQASLEYEHQRESSQLLKDKONEVKOHFONLEYAKKELDKERNLLDQQKK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 QELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----OLREEQVRF---LEKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 VDSEAIFQLKEKVAQERKELEELYLVKKQKQDQKENELLFFEKQLKQHQADFENELEAKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EK-----ALKELTESQEAVQAMMSSVTELRTNLN----ALKELITENKTVIEQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 RLSDFGDRLEANTGDFTALIADFQLSLE------EFKS-VGTKVETMLSP---F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Citron protein (Rho-interacting, serine/threonine kinase 21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1805;
```

S

015492;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8,
                                                                  SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: A MAJOR SIGNAL WAS OBSERVED IN TESTIS AND
BRAIN, BUT IT WAS ALSO DETECTED IN THYMUS, SPLEEN, KIDNEY, HEART
                                     -I- FUNCTION: PUTATIVE RHO/RAC EFFECTOR THAT BINDS TO THE GTP-BOUND FORMS OF RHO AND RACI. IT PROBABLY BINDS P21 WITH A TIGHTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHMKQQ---IQQFGEENTRLHTAVENLKAVNVELSEQI------NQLKQLHTRLS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNMKAQEEMISELRQOKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKSRLLELETRLR 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 DFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFE-KLAQS---LKETF--SQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 -----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAVQAMMSSVTELRTNLNALKE---LITENKTVIEQLKAD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 ANDEIVQLRSE-VDHLRREITEREMQLTSQRQTMEALKTTCTMLEEQVLDLEALNDELL
daule P., Furuyashiki T., Reid T., Ishizaki T., Watanabe G., ril N., Narumiya S.; novel partner for the GTP-bound forms of rho and rac."; B. Lett. 377:243-248(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1597;
                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-LYS.
PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3-BINDING (POTENTIAL)
W; 7B7286C2305676DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                             coil; Phorbol-ester binding; SH3-binding.
1 845 COILED COIL (POTENTIAL).
674 870 RHO/RAC BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 138.5;
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0419; DAG_PE_BIND_DOW_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1
                                                                                                                                                                                                                            EMBL, U39904; AAC52341.1; --
MGD; MGI:105313; C1t.
InterPro; IPR001180; CNH.
InterPro; IPR001219; DAG_PE-bind.
InterPro; IPR001849; PH.
InterPro; IPR000861; REM_repeat.
Pfam; PF00130; DAG_PE-bind; I.
Pfam; PF00130; DAG_PE-bind; I.
SMART; SM00109; C1; I.
SMART; SM00109; C1; I.
SMART; SM00233; PH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183448 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.8%;
                                                          SPECIFICITY IN VIVO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                 BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1521
                                                                                                                                                                                                                                                                                                                                                                                                                         931
1011
1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                 Coiled
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
MYH3_HUMAN
ID MYH3 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
$$$££3888888888888888888888
```

1940 AA.

PRT;

STANDARD;

MYH3_HUMAN

ð 셤 à q à a õ g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 856-1940 FROM N.A.

MEDLINE-8936648; PubMed-2771643;

Rarsch-Mizzachl I., Travis M., Blau H., Leinwand L.A.;

Rarsch-Mizzachl I., Travis M., Blau H., Leinwand L.A.;

Rarsch-Mizzachl I., Travis M., Blau H., Leinwand L.A.;

Expression and DNA sequence analysis of a human embryonic skeletal

muscle myosin heavy chain gene.";

Nucleic Acids Res. 17:6167-6179(1989).

- I- FUNCTION: MUSCLE CONTRACTION: A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MIC). 2 ALKALI LIGHT CHAIN SUBUNITS (MIC).

- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MUSCLE

- NUCLE OF THE STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MUSCLE

- NUCLE OF THE STAGE: ABUNDANTLY PRESENT IN HEART AND ADULT SKELETAL
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic (Muscle embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
-1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLAPED AND ARE REDOITED FOR WYOSIN ATPASE ACTIVITY.
-1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT BEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of three developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                           Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9003298; PubMed-2806546;
BILET M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
Raychowdhury M.K., Rubinstein N.A. Kelly A.M., Sarkar S.;
"Human embryonic myosin heavy chain cDNN. Interspecies sequence
conservation of the myosin rod, chromosomal locus and isoform
peperitic transcription of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H.,
Rubinstein N.A., Kelly A.M., Sarkar S.;
"Nucleotide sequence of full length human embryonic myosin heavy
chain cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
MEDLINE-90235862; PubMed-1691980;
Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 17:3591-3592(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89263803; Pubmed-2726495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myosin heavy chains.";
Eur. J. Biochem. 189:55-65(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 856-1940 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13988; CAA32167.1; -.
                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
```

```
Local Similarity
nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324 NKAKNALAHALQSSRHDCDLLREQYEEEGEGKAELQRALSKANSEVAQWRTKYETDAIQR 1383
                                                                                                                                                                                                                                                                                                                                                                                                       282 BEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQP 341
                                                                                                                                                                                                                                                                                                                                                                                             171 LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQ---- 226
                                                                                                                                                                                                                                                                                                                                                           121 TPSQVVRHMKQQ-----IQQFGEENTRLHTA-VENLKAVN----VELSEQINQLKQLHTR 170
                                                                                                                                                                                                                                                                                                                                             33; Gaps
                                                                                                                                                              Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                               227 -EAVQAMMSSVT----ELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL
                                                                                                                                                                                                                                                                                                                          Length 1940;
                                                                                                                                                                                                                 ATP (POTENTIAL).

ACTIN-BINDING.

ACTIN-BINDING.

ACTIN-BINDING.

ALKYLATION (TRI-1).

ALKYLATION (SH-1).

ALKYLATION (SH-2).

A -> G (IN REF. 3).

KK -> QE (IN REF. 3).

SR -> RA (IN REF. 3).

RG -> QT (IN REF. 3).

RG -> QT (IN REF. 3).

RG -> QT (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cr-1989 (Rel. 12, Created)
01-0cr-1989 (Rel. 12, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                                                                     IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            7.9%; Score 136.5; DB 1;
21.4%; Pred. No. 1.9;
Live 56; Mismatches 102;
                                                                                                                                                                                           MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1940 AA
                                                                                      Pfam; PF00612; IQ; 2.
Pfam; PF00613; myosin_head; 1.
Pfam; PF00736; Myosin_k; 1.
Pfam; PF01765; Myosin_ki; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
SMART; SM00142; MYS: 1.
PROSITE; PS50096; IQ; 1.
                                                                         IPR002928; Myosin_tail.
IPR001609; myosin_head.
      EMBL; X13100; CAA31492.1; -.
EMBL; X51593; CAA35942.1; -.
EMBL; X15696; CAA33731.1; -.
PIR; S04090; S04090.
HSSP; P08799; IMMD.
                                                                Myosin_N.
                                                                                                                                                                                                                                                                                                       224035
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYH3.
Rattus norvegicus (Rat).
                                                        InterPro; IPR000048; IQ.
InterPro; IPR004009; Myo
                                                                                                                                                                                                                                                             706
1331
1392
1609
                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                      Multigene family.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1384 TEE 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 QDE 344
                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYH3_RAT
                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                   InterPro;
                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12847;
                                                                                                                                                                                                      DOMAIN
DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                              MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DT DT DT OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                            KW
FT
FT
FT
FT
FT
FT
FT
FT
FT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            AND. BIOL. 190:291-317(1986).

AND. BIOL. 190:291-317(1986).

C. I- FUNCTION. MUSCLE CONTRACTION.

C. I- SUBGNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2. HEAVY CHAIN SUBUNITS (MLC.).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC.2).

C. I- SUBCELLUIAR LOCATION: THICK filaments of the myofibrils.

C. CYCLES OF A 28-RESIDUE REPART PATLES OF SEPTITIVE, SHOWING

C. CYCLES OF A 28-RESIDUES REPART PATLES COLLED COLLES.

CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

C. PTM: TWO CYSTEINE RESIDUES IN THE SIDOMAIN ARE SELECTIVELY

ALKULTATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

C. HIGGELANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LAM) AND 1 HEAVY MEROMYCSIN (HMM). IT CAN LATER BE

MEROMYOSIN (LAM) AND 1 HEAVY MEROMYCSIN (HMM). IN CONTAINS 1 WOSIN-LIKE GLOBULAR HEAD DOMAIN.

C. SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coil; Thick filament; Actin-binding;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                         Strehler E.E., Strehler-Page M.-A., Perriard J.C., Periasamy M., Nadal-Ginard B., "Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
Myssln, wuscle protein; Colled coil; Thick filament; Actir calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKYLATION (SH-2).
W; B5D546A596E5A696 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQ.
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 136.5; L
llarity 21.4%; Pred. No. 1.9;
Conservative 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 From PF00612: 10; 2.

Pram; PF00613; myosin_head; 1.

Pram; PF01736; myosin_hi

Pram; PF01576; Myosin_tail; 1.

PRINTS; PR00193; MYOSINHEAVY.

ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08799; 1MND.
InterPro; IPR0000048; IO.
InterPro; IPR002028; Myosin_N.
InterPro; IPR002028; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87060988; PubMed=3783701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04267; CAA27817.1; -. PIR; A24922; A24922.
                                                                                                                                                                                                                                                                                                 myosin heavy chain gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   782
840
179
656
758
130
696
706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
```

7;

Gaps

33;

Indels

101;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way entities requires a license agreement is no removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                     1264 NEETQRSLSELTTQKSRLQTEAGELSRQLEEKESIVSQLSRSKQAFTQQIEELKRQLEEE 1323
                                                                                                                                                                                                                1324 NKAKNALAHALOSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDALQR 1383
121 TPSQVVRHMKQQ-----IQQFGEENTRLHTA-VENLKAVN----VELSEQINQLKQLHTR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq. 7:71-82(1997).
Seq. 7:71-82(1997).
Seq. 7:71-82(1997).
Seq. 7:71-82(1997).
TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY DETECTABLE MALE ANTICEN (SDM).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN EXOUND IN SPERMATIDS DURING SPERMATOGREESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
                                                            171 LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQ----
                                                                                   -EAVQAMMSSVT----ELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRQEL
                                                                                                                                                                                     282 EEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CD-1; TISSUE-Testis;
MEDLINE-97217683; PubMed-9063644;
Kondo M., Sutou S.;
"Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ALA.
W; 3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Golgin-160 (Male-enhanced antigen-2) (MEA-2).
                                                                                                                                                                                                                                                                                                                                                                   1325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatogenesis; Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149880 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D78270; BAA19612.1; -. HSSP; P18852; 1SCG.
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:96958; Golga3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 20
1325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 1384 TEE 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoantigen.";
DNA Seq. 7:71-
                                                                                                                                                                                                                                                   342 QDE 344
                                                                                                                                                                                                                                                                                                                                                              G160_MOUSE
P55937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                           1216
                              g
                                                                                      g
                                                             à
                                                                                                                         ò
                                                                                                                                                      合
                                                                                                                                                                                  ò
                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                  ð
```

```
126 VRHMKQQIQQ----FGEENTRL-----HTAV------ENLKAVNVELSEQIN----- 162
                                                                                                                                                                                    243 LNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLL 302
                                                                                                                                                                                                          Esser K., Tidhar A., Myszkowski M.;
"Isolation and characterization of the human perinatal MHC promoter.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
MEDLINE-95324556; PubMed-7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S., Stedman H.H., Rubinstein N.A.;
                          405 LOHAROWYQQQLTLAQEARVRLQGEMAHIQVGQMTQAGLLEHLKLENVSLSHQLTETQHR
                                                            -----QLKQLHTRLSD----FGDRLEANTGDFTALIADFQLSLEEFKSVGTKVET
                                                                                   465 SIKEKERIAVQLQSIEADMLDQEAAFVQIREAK----TWVEEDLQRRLEEFEGEREQLQK
                                                                                                                              ------TFSQEAVQAMMSSVTELRTN
                                                                                                                                                      521 VADAAAASLEQQLEQVKLTLFQRDQQLAALQQEHLDVIKQLTSTQEALQAKGQSLDDLHTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a developmentally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                        P1355; 014910; Created)
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Skeletal muscle;
MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
"Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arnold H.H.; "Identification of three developmentally controlled isoforms of myosin heavy chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of a human perinatal myosin heavy-chain
                                                                                                                                                                                                                                                303 KDSTINLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQ 346
                                                                                                                                                                                                                                                                       PRT; 1937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 230:1001-1006(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feghali R., Leinwand L.A.;
"Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skeletal muscle;
MEDLINE-90235862; PubMed-1691980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 860-1937 FROM N.A.
MEDLINE-89234168; PubMed-2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Blochem. 189:55-65(1990).
                                                                                                                           MLSPFEKLAQSLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 502-1937 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5]
SEQUENCE OF 1-46 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 89:289-294(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcript
                                                             163
                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                             MYH8_HUMAN
                         g
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                     g
                                                                                                                        ò
                                                                                                                                                      g
                                                                                                                                                                                                                  g
                                                                                                                                                                                  ογ
                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                            q
```

6

Gaps

78;

DB 1; Length 1325;

7.8%; Score 136; DB 1; Length 13 23.6%; Pred. No. 1.3; tlve 38; Mismatches 101; Indels

Conservative

Query Match Best Local Similarity Matches 67; Conserv

6

Gaps

```
USO1_YEAST
                                                                                                                                                   181
                                                                                                                                                                                                                                                      230
Matches
                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-1).

SUBCELLUIAR LOCATION: Thick filaments of the myofibrils. SHOWING DOWAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING DOWAIN: THE ROBLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

PHY: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLAPED AND ARE REQUIRED FOR MYOSIN ATBASE ACTIVITY.

ALKYLAPED AND ARE REQUIRED FOR MYOSIN AREAS ACTIVITY.

MISCELLANGOUS. EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM). AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SELLY PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIN LITER ACTIN CONTROLL ACTIN LITER ACTIN CARL CONTROLL ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
A -> R (IN REF. 2).
E -> Q (IN REF. 2).
M -> M (IN REF. 1 AND 4).
N -> H (IN REF. 1 AND 4).
E -> G (IN REF. 1 AND 4).
K -> DGG (IN REF. 1 AND 4).
K -> DGG (IN REF. 1 AND 4).
K -> M (IN REF. 1 AND 4).
K -> M (IN REF. 3).
E -> G (IN REF. 1 AND 4).
K -> M (IN REF. 3).
EN -> AH (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                       -: SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A3EE2D151792E9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Colled coil; Thick filament; Ac
ATP-binding; Methylation; Alkylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> D (IN REF
-> H (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EN -> D -> H -> D -> H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pfam, PF00736; Myosin_N; 1.
Pfam, PF00736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODom; PD0000355; myosin_head; 1.
SMART; SM00215; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR004009; Myosin_N.
Interpro; IPR002928; Myosin_tail.
Interpro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51592; CAA35941.1; -. EMBL; M35250; AAA36346.1; -. EMBL; AF067143; AAC21557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M36769; AAC17185.1; -. EMBL; Z38133; CAA86293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1261
1297
1378
1505
1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A30220; A30220.
HSSP; P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1504
1847
1914
1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
261
297
377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z38133;
EMBL; X51592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 160741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD
                                                                                                                                                                                                                                                      ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KA SUBARAN SUB
                        888888888888888888888
```

DB 1; Length 1937;

Score 135.5; Pred. No. 2.2;

7.8%;

Query Match Best Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRARES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILLS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bal Y., Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
                                                                                                                                                                                                                  1249 EKMCRSLEDQVSELKTKEEEQQRLINDLTAQRARLQTEAGEYSRQLDEKDALVSQLSRSK 1308
                                                      1133 AKAEKQRSDLSRELEEISERLEE-AGGATSAQVELNKKREAEFQKLRRDLEEATLOHEAM 1191
                                                                                                                                                                                        QA------MASSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL 281
                                                                                                                                                                                                                                                                    282 BEACSTLSHSIATL----QESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDD 337
                               130 KQQIQQFGE----ENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEA---- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A cytoskeleton-related gene, usol, is required for intracellular protein transport in Saccharomyces cerevislae."; J. Cell Biol. 113:245-260(1991).
                                                                                                             ----NTGDFTALIADFQLSLEEFKSVGTKVETML----SPFEKLAQSLKE-TFSQEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
11-docellular protein transport protein USO1
0501 OR INTI OR YDL058W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1790 AA.
  48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91185402; PubMed=2010462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 782-1790 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54378; CAA38253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-8 FROM N.A.
    56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                         1309 OASTO 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kendrick K.E.;
                                                                                                                                                                                                                                                                                                                                                                   338 SAQPQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USO1_YEAST
```

```
1372 LNEGS-STITQEYSEKINTLEDELIRLQNENE-LKAREIDNIRSELEKVSLSNDELLEEK 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE--ESSKEKAELEKSKEMMKKLESTIESNETELKSSMETIRKSDEKLEQSKKSA---EE 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1545 DIKNLOHEKSDLISRINESEKDIEELKSKLRIEAKSGSELETVKGELNNAGEKIRINAEE 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
MEDLINE-99318869; PubMed-10388558;
MALSA A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the complete human sarcomeric myosin J. Mol. Biol. 290:61-75(1999).

-I- FUNCTION: MUSCLE CONTRACTION.
-I- SUBUNIT: MUSCLE MYOSIN IS A HEXAMBRIC PROTEIN THAT CONSISTS OF 2
                                                                                                               Golgi stack; Cytoskeleton; Coiled coil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 INQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFK-----SVGTKVETMLSPF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LSEQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 QVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVM--VQDGAES 327
                                                                                                                                     COLLED COIL (POTENTIAL).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FUNCTION.

ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

Y -> I (IN REF. 2).

Y -> I (IN REF. 2).

Y -> I (IN REF. 2).

Y -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                   36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, fetal (Myosin heavy chain IIb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 EKLAQSLKETF----SQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 1; Length 1790;
Pred. No. 2.5;
3; Mismatches 121; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                   117 IRDGTPSQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVE-----
                                                                                                                                 HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1939 AA.
                                                                                                                             GLOBÜLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1605 NTVLKSKLEDIERELKDKQAEIKSNQE 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STVEEASQDDSAQPQDENQSDAGEHKD 354
                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                         SGD; S0002216; USO1.
InterPro; IPR002017; Spectrin.
                                                                                                               transport;
EMBL, L03188; AAB00143.1; EMBL, U53668; AAB66659.1; PIR; A38455, A38455.
                                                                                                                                                                                                                                                                                                                1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                         57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                         Transport; Protein
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   1772
1790
                                                                                                                                                                                                                                                                      1581
1600
1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYH4_HUMAN
Q9Y623;
                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Best Local (
Matches 5.
                                                                                                                                                     DOMAIN
                                                                                                                                                                    DOMAIN
                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328
                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ώ ώ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLLUALE LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFILDES, PTM: TWO CYSTEINER RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT SPLIT EURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1161 TSAQIELNKKREABFQKMRRDLEESTLQHEATAAALRKKHADSVABLGKQIDSLQRVKQK 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1221 LEKEKSELKMEINDLASNMETVSKAKANFEKMCRTLEDQLSEIK----TKEEEQORLIN 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TPSQVVRHMK-----QQIQQFGEENTRLH----TAVENLKAVNV-ELSEQINQLKQLHTR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 SIATLQESTTLLKDSTTNLHAVESRLIGVMYQDGAESSTVEEASQDDSAQPQDENQ---- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 AMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1939;
                                                                                                                                                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
W; 40BlAD1D777A47DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. No. 2.9;
Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7%; Score 133.5;
20.4%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR0042028; Myosin_Lail.
InterPro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 2.
Fram; PF00613; myosin_head; 1.
Fram; PF01776; Myosin_Lail; 1.
Fram; PF01776; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODDm; PD0001355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF111783; AAD29949.1; -. HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FroDom; PD000055, IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM0242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || || ::
1396 KLAQRLQDAEEHVEA 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814
1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                843 193
179 18
1939 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 160742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sim
Matches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

RESULT 13

```
433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 19.1%;
nes 48; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z35308; CAA84549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
         STANDARD;
                                                                                                                                                                                                                                               Haloarcula vallismortis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 DSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00304; HAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 QSASIEEVSDS 396
                                                                                                                                                                                                                                                                                      Archaea; Euryarch;
NCBI_TaxID=28442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
MYS3_HYDAT
ID MYS3_HYDAT
                HTR2_HALVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏλ
                SOT TWO PROPERTY AND PROPERTY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREGVRFLEKRKQEL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 VRHMKQQIQQFGEENTRLHTAVENLKAVNVELSE-----QINQLKQLHTRLSDFG-DRL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 IKKIEEELKRTTEEERKLRV---NLRKLEIKLREFSVMRDIAEQIKELESKLKGFNLEEL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 EANTGDFTALIADFQ-----LSLE------EFKSVGTKVETMLSPFEKLAQSLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POKEREFEGINEEFNKIKGELIGLERDIKRIKALEGRRKIJEEKVRAKEELENIHRQIR 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and evolution.";
Submitted (Jur.1999) to the EMBL/GenBank/DDBJ databases.
Submitted (Jur.1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
-i- FUNCTION: Involved in DNA double-strand chandounclease activity
and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of mrell by unwinding
and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome. NP_BIND 30 31 ATP (BY SIMILARITY). DOMAIN 144 745 COILED COIL (POTEWTIAL). SEQUENCE 880 AA; 103970 MW; FDB177EC7E026479 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 EEACSTLSHSIATLQESTTLLKDSTTNLHAVE-----SRLIGVMVQDGAESSTVEE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 133; DB 1; Length 880; 23.3%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: Forms a complex with mrell (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :68
                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 AFPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                           880 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR001238; RecF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ248286; CAB50131.1; -.
                                                                                                                                                                                           (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00470; RecF;
SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                      RAD50 OR PAB0812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                    RA50_PYRAB
Q9UZC8;
```

Query Match Best Local

Matches

g οy QQ ŏ

ò

522 222

> qq δ

RESULT 14 HTR2_HALVA

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 IDRATEEQARTAQDVMGTIDDLTTISQCTAT------EADTVAGAAQD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 RKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 FGD------RLEANTGDFTALIAD-----FQLSLEBFKSVGTKVETMLSPFEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 IEAIQEQ-AGDIVETMESISTRITEGVSTVEETVDALETIVE-----YTEEVDTGIQE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 TAIRDGTPSQVVRHMKQQIQQFGEENTR-LHTAVENLKAVNVELSEQINQLKQLHTRLSD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 TAOQVASSAQQVADTSQSAAKVGEDGREAAQEAIAEMSAIEAETGETVEEINALDDELDE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 IGEIVGVITSIVEQTNMLALNASIEÄAHÄDGDGEGFAVVADEIKGLAEETKEAAADIEGR 291
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sensory rhodopsin II transducer (HTR-II) (Methyl-accepting phototaxis
protein II) (MPP-II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additional retinal protein subgroup is coexpressed with its additional retinal protein subgroup is coexpressed with its proc. Natl. Acad. Sci. U.S.A. 92:3086-3040(1995).
- POWCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN II (SR-II) TO THE FLAGELLAR MOTOR. RESPONDS TO SENSORY RHODOPSIN II (SR-II) TO THE FLAGELLAR MOTOR. RESPONDS TO SENSORY HONORS THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
                                                                                                                                                                                                                                  Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 433;
                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
STRAIN=ATCC 29715;
SERDINE-ATCC 29715;
MEDLINE-82224074; PubMed-7708770;
Seidel R., Scharf B., Gautel M., Kleine K., Oesterhelt D.,
Engelhard M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER 1 1
SEQUENCE 433 AA; 45935 MW; 90507B8897D943C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ransducer; Photoreceptor; Transmembrane; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of sensory rhodopsin II: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 132; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004089; Chemotaxis_transducer
InterPro; IPR003660; HAMP.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                     SEQUENCE FROM N.A.

Nakano M.Y., Stidwill R.P.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

SUBMITTION: WYOSIN IS A PROTEIN HAT BINDS TO F-ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

TO OTHER NON MUSCLE MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 KEGLESQ-ISQLQRKIQELLAKIEELEEELENERKLR-QKSEL--QRKELESRIEELQDQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 RDGTPSQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 LETAGGATSAQV-----EVGKKREAECNRLRKEIEALNIANDAAISAIKAKTNA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 TFS--QEAVQAMMSSVTELRTNLNALKELITENKTVIEQLK-----ADAQLREEQVRF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 LEKRKQELEE-----ACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 LNSKLAQVDELHSQSESKNSKVNSELLALNSQLSESEHNLGIATKNIKTLESQL----- 515
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
Myosin; Muscle Protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding.
1 1
DOMAIN <1 38
        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OZT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, clone 203 (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 7.6%; Score 132; DB 1; Length 539; Best Local Similarity 23.2%; Pred. No. 0.76; Matches 62; Conservative 51; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1 38 GLOBULAR HEAD.
39 >539 RODLIKE TAIL.
39 520 COILED COIL (POTENTIAL).
539 539 WW; 9C5AD5664060939D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 LEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 DGAESSTVEEASODDSAQPQDENQSDA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AESKNFNEA--ESKAKLENYNSSNA 538
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L35595; AAA29216.1; -.
HSSP; P24733; 1WDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g g
```

Search completed: August 13, 2002, 09:30:42 Job tlme: 378 sec



Appii Appii Appii Appii Appii Appii Appii Appii

```
113 VITAIRDGTP----SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 LHTRLSDFGDRLEANTG-DFTALIADFQLSLEEFK----SVGTKVETMLSPFEKLAQSLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIVQEEQIVELIEKIGAVEEELNRVTELFMDNKNELDQCKSDLQNKTQELETTQKHLQET 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ETFSQEAVQAMMSSVTELRINLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            882 EEACSTLSHSIATLQES--TTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Seq
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.1%; Score 140; DB 4; Length 1057;
Best Local Similarity 21.7%; Pred. No. 0.00047;
Matches 56; Conservative 56; Mismatches 100; Indels 4(
                             SQUENCE 10, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: NASLOW, COREY
APPLICANT: SAKOWICZ, ROMAN
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT FILING DATE: 2000-04-03
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08328254
Patent No. 5710022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DSAQPQDENQSDA 349
 | : |:::|
513 LHSKLDRKKAVDQHNAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: H.sapiens
US-09-541-782-10
   JS-09-541-782-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1057
109
108.5
108.5
107.5
107.5
107.5
107.5
106.5
106.5
106.5
106.5
106.5
106.5
106.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                        Search time 23.55 Seconds (without alignments) 368.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl1
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Appl
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                             1733
1 MTVSTDNTSPVISRASSPTF......DDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jescription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seduence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgg2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/RB_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/RB_COMB.pep:*
   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-592-126-148
US-08-687-080-51
US-08-53-306A-2
US-08-742-923A-2
US-08-085-199B-11
US-08-685-871-2
US-09-067-351-1
US-09-685-576-4
                                                                                                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-452-294-1
PCT-US93-06160-4
US-09-541-782-2
US-08-591-079-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-353-700-1
PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-466-390-4
US-08-470-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-328-254-7
US-08-685-576-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-195-487-4
US-08-483-924-4
                                                                                                                                                                                                                                                                                                  231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-480-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
                                                                                                         August 13, 2002, 09:21:49
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                    Manimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                              US-09-673-763-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                    OM protein
                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
N
```

10;

Gaps

```
TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RKQELEEACSTLSHSIATLQESTT----LLKDST----
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED. JANETE: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                    TITLE OF INVENTION.

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 LRINLNALKELITENKTVIEQLKADAQLREEQVRFLEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 131; DB 1; ilarity 21.9%; Pred. No. 0.016; Conservative 44; Mismatches 92.
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: HUMAN US-08-353-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>2</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | ::|| || |: | :| || 332 L--NKREIEELTQENGTLKE---INASLNQEKMNLIQKSESFANYIDEREKSISELSDQY 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 KQEKLILLORCEETGNAYEDLSOKYKAAQEKNSKLECLLNECTSLCENRKNELEQLKEAF 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LE----EFKSVGTKVETMLSPFEKLAQS------LKETFSQEAVQAMMSSVTE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 NTRLHTAVENLKAVNVELSEQINQLKQLH----TRLSDFGDRLEANTGDFTALIADFQLS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                         APPLICANT: Zhu, Xueliang
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVORTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 -----TNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQSDAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 131; DB 1; Length 2482;
21.9%; Pred. No. 0.011;
Live 44; Mismatches 92; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RKQELEEACSTLSHSIATLQESTT----LLKDST----
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEK------
                                                                                                                                         E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A. RECISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08353700 Patent No. 5599919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 21.9 Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                  STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                             GENERAL INFORMATION:
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-353-700-1
                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

```
Sequence I. Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Yen, Jerome B.
APPLICANT: Nathor, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                  964 L--NKREIEELTQENGTLKE---INASLNQEKMNLIQKSESFANYIDEREKSISELSDQY 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1019 KQEKLILLQRCEETGNAYEDLSOKYKAAQEKNSKLECLLNECTSLCENRKNELEQLKEAF 1078
                                                                                                         140 NTRLHTAVENLKAVNVELSEQINQLKQLH----TRLSDFGDRLEANTGDFTALIADFQLS 195
                                                                                                                                                                                                                                                                            92; Gaps
                                                                                                                                                                      846 NSDLQKQCEELVQIKGEIEENLMKAEQMHQSFVAETSQRISKLQEDTSAHQNVVAETLSA
                                                                                                                                                                                                                              196 LE----EFKSVGTKVETMLSPFEKLAQS------LKETFSQEAVQAMMSSVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 AKEHQEFLTKLAFAEERNONLML----ELETVQQALKSEMTDNONNSKSEAG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQSDAG 350
Length 3248;
                                                             Indels
```

10;

```
2101 amino acids
              ADDRESSEE: TESTA, HURWI
STREET: 125 HIGH STREET
                                                                                                        ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                            USA
                                                  BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                    CITY: BO:
STATE: MACCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-466-390-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019 KQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNECTSLCENRKNELEQLKEAF 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 NTRLHTAVENLKAVNVELSEQINQLKQLH----TRLSDFGDRLEANTGDFTALIADFQLS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 LE----EFKSVGTKVETMLSPFEKLAQS-------LKETFSQEAVQAMMSSVTE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906 LENKEKELQLLNDKVETEQAEIQELKKSNHLLEDSLKELQLLSETLSLEKKE--MSSIIS 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 AKEHQEFLIKLAFAEERNQNLML----ELETVQQALRSEMIDNQNNSKSEAG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08466390
Patent No. 5686562
GENERAL INFORMATION:
APPLICANT: TOURATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 -----TNLHAVESRLIGVMYQDGAESSTVEEASQDDSAQPQDENQSDAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 131; DB 5; Length 3248; Best Local Similarity 21.9%; Pred. No. 0.016; Matches 64; Conservative 44; Mismatches 92; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 -----RKQELEEACSTLSHSIATLQESTT----LLKDST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 LRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEK------
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US95/16216
                      Herrell and Skillman
t Suite 720
                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATONNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
RECISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                    ADDRESSEE: Dann, Dorfman, H
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
PCT-US95-16216-1
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-466-390-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
```

ò a

```
128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 HFEEEKQQLSSLITDLQSSISNLS----QAKEELEQASQAH-----GAKLTAQVASLTS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 ELTTLNATIQOQDQELAGLKQQAKEKQA---QLAQTLQQ--QEQASQGLRHQVEQLS--- 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-08-470-950-4

Sequence 4, Application US/08470950

Patent No. 5698439

GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY

APPLICANT: LIDGARD, GRAHAM P

TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE

VUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT

CITY: BOSTON
STREET: 125 HIGH STREET
CITY: MA

COUNTRY: USA

ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 DSTINLHAVESRL-IGVMVQDGAESSIVE------EASQDDSAQPQDENQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.3%; Score 126; DB 1; Length 2101; Best Local Similarity 22.5%; Pred. No. 0.024; Matches 55; Conservative 48; Mismatches 97; Indels 4
                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
RECISTRATION NUMBER: WTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
HURWITZ & THIBEAULT
                                                                                                                           COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOCK-TRADE: PATTER
```

ő

```
APPLICATION NUMBER: US/08/46 FILING DATE: 06-JUN-1995 CLASSIFICATION: 424 ATTORNEY AGENT INFORMATION: NAME: PITCHER ESQ, EDMUND R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672 QVAE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΜĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --EASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TOUGHTLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 126; DB 1; Length 21C Best Local Similarity 22.5%; Pred. No. 0.024; Matches 55; Conservative 48; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                 NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/COCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO.
INFORMATION FOR SEQ ID NO.
LINGOMATION FOR SEQ ID NO.
LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSTINLHAVESRL-IGVMVQDGAESSTVE--
                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08467781; Patent No. 5780596; GENERAL INFORMATION:
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-470-950-4
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                    FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 QVAE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
```

```
128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                      456 HFEEEKQQLSSLITDLQSSISNLS----QAKEELEQASQAH-----GARLTAQVASLIS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 DSTINLHAVESRL-IGVMVQDGAESSTVE------EASQDDSAQPQDENQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::||: :|| |::| | :|: | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | |
                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
COURSERONDENCE: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   7.3%; Score 126; DB 1; Length 2101; 22.5%; Pred. No. 0.024; Live 48; Mismatches 97; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/195,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TESTA HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08195487; Patent No. 5783403; GENERAL INFORMATION:
                  REGERENCE/DOCKET NUMBER: MTP-
REFERENCE/DOCKET NUMBER: MTP-
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
27,829
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.55
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
REGISTRATION NUMBER:
                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109
```

6

us-09-673-763-8.rai

```
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 QVAE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-452-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                 128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                      184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                   456 HFEEEKQOLSSLITDLQSSISNLS----OAKEELEQASQAH-----GARLTAQVASLTS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                            244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 SSLKQKEQQLKEVAEKQEATRQDHAQQL-----ATAAEEREASLRERDAALKQLEALEK 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 DSTINLHAVESRL-IGVMVQDGAESSTVE------EASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                               Query Match
7.3%; Score 126; DB 1; Length 2101;
Best Local Similarity 22.5%; Pred. No. 0.024;
Matches 55; Conservative 48; Mismatches 97; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
              NAME: PITCHER ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEFHOME: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08483924; Patent No. 5882876; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          ; MOLECULE TYPE: protein
US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 125 H
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      672 QVAE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02110
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-08-483-924-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09452294
Patent No. 6287790
GENERAL INFORMATION:
APPLICANT: Lelievre, Sophie
APPLICANT: Lelievre, Sophie
APPLICANT: Bissell, Mina
TITLE OF INVENTION: UTILIZATION OF NUCLEAR STRUCTURAL PROTEINS FOR TARGETED
TITLE OF INVENTION: THERRHAND DETECTION OF PROLIFERATIVE AND
TITLE OF INVENTION: DIFFERENTIATION DISORDERS
FILE REFERENCE: IB-1454 - Sequence Submittal
Patent No. 6287790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 DSTINLHAVESRL-IGVMVQDGAESSTVE------EASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 HFEEEKOOLSSLITDLOSSISNLS----OAKEELEOASOAH-----GARLTAOVASLTS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSYTELRTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||: :| | |::|| | |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44:
                                                                                                                                                                                                                                                                                                                                                                             Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.3%; Score 126; DB 4; Length 2101; Best Local Similarity 22.5%; Pred. No. 0.024; Matches 55; Conservative 48; Mismatches 97; Indels 4.
                                                                                                                                                                                                                                                                                                                                        Query Match 7.3%; Score 126; DB 2; Length 21/
Best Local Similarity 22.5%; Pred. No. 0.024;
Matches 55; Conservative 48; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/452,294
CURRENT FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/110,420
PRIOR FILING DATE: 1998-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.1
                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-924-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-452-294-1
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
```

QΥ g ò

```
LSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 DGTPSQVVRHMKQQIQQFGEENTRLHTAVENL-----KAVNVELSEQINQLKQLHTR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 LSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFFKLAQSLKETFSQEAVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AMMSSVTELRTNLNALKELITENKTVIEQLKADAQLRE---EQVRFLEKRKQELEEACST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08591079
Patent No. 5972899
GENERAL INFORMATION:
APPLICANT: Zyohlinksky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella IpaB
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CONTRADABE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 125.5; DB 4;
19.8%; Pred. No. 0.011;
tive 59; Mismatches 111;
                                                                                                                                                                                                                       APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NOS: 10
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue,
                                                                                                                                               Sequence 2, Application US/09541782 Patent No. 6284480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: A. nidulans
US-09-541-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GRYRDA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 DAGEHKDS 355
            672 QVAE 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE.
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-591-079-2
                                                                                                      RESULT 12
US-09-541-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 òχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 HMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEAN----TG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 HFEEEKQQLSSLITDLQSSISNLS----QAKEELEQASQAH------GARLTAQVASLTS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 DFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 NALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLKQKEQQLKEVAEKQEATRQDHAQQL-----ATAAEEREASLRERDAALKQLEALEK 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Gaps
                                                                                                                   : : : : : | : : | | : : | | : : | | | : : | | | | : : | | | | | : : | | | | : : | | | | : : | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | | : : | | | | : : | | | | : : | | | | | : : | | | | : : | | | | | : : | | | | : : | | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | : : | | | : : | | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | 
                        611
                                                                                 -----EASQDDSAQPQDENQS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOVEL MALIGNANT CELL TYPE MARKERS OF THE INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 126; DB 5; Length 21
22.5%; Pred. No. 0.024;
tive 48; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL MALIGNANT CEITLE OF INVENTION: INTERIOR NUCLEAR MAITTILE OF INVENTION: INTERIOR NUCLEAR MAINER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA HURMITZ & THIBEAULT STREET 53 STATE STREET
                                                                                          304 DSTINLHAVESRL-IGVMVQDGAESSTVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSTINLHAVESRL-IGVMVQDGAESSIVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9306160 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-C
TELECOMMUNICATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INPORMATION: POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101
      ::||: :| ::|:
558 SSLKQKEQQLKEVAEKQEATRQDHAQQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%
Best Local Similarity 22.5%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19930621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein -US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: BOSTC
STATE: MA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02109
                                                                                                                                                                                                                                                                         672 QVAE 675
                                                                                                                                                                                                                348 DAGE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506
```

οy Pp δλ

qq οy g

;

Gaps

Length 1184;

```
;
;
                                                                                                                                                                                                                                                                                                                      139 ENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEE 198
                                                                                                                                                                                                                                                                                                                                                   394 BOQRLEKNEDQLKILTMELQKKSSELEEM------TKLTNNKEVELEE 435
                                                                                                                                                                                                                                                                                                                                                                                                       199 FKSVGTKVETML---SPFEKLAQSLKETFSQEAV---QAMMSSVTELRTNLNAL----- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                  247 -----KELITE-----NKTVIE-----QLKAD--AQLREEQVRFLEKRKQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 ELEEACSTLSHSIATLQESTTLLKDS------TTNLHAVESRLIGVMVQDG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 E----ERMLKQIENLQETETQLRNELEYVREELKQKRDEVKCKLDKSEENCNNLRKQVE 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-328-254-7
Sequence 7, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Xuellang
APPLICANT: Lee, Wan-Hwa
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                        6.9%; Score 119; DB 4; Length 976; 23.5%; Pred. No. 0.033; tive 37; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: DE-DOS/MS-DOS
SOCTUMENE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBOBLI, CASTANYA
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION: MEPERICOMMUNICATION:
METERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION: MEPERICOMMUNICATION:
METERENCE/DOCKET NUMBER: P-CJ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                        | TELEPHONE: (212) 318-3000
| TELEFAX: (212) 752-5958
| INFORMATION FOR SEQ ID NO: 4:
| SEQUENCE CHRRACTERISTICS:
| LENGTH: 976 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| US-09-104-3248-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9049
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERIZICS:
LENGTH: 180 amino acids
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.5%
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 AESSTVEEASQDDSA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 NKNKYIEELQQENKA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92122
                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09104324B
Patent No. 6232460
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: T recl. Ozlem; Sahin, Ugur; Pfreundschuh, Michael
TITLE OF INVENTION: Methods For Diagnosis And Treating Cancers,
TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers In A Sample Of
TITLE OF INVENTION: No. 6232460mal Cells
TORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 SQVVRHMKQQIQQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLAQSL-----KETFSQEAVQAMM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 SQLTLLIGNLIQILGEKSL---TALTN-KITAWKSQQQARQQKNL----EFSDKINTLL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 SSVTELRTNLNALKELITENKTVIEQ--LKADAQLREEQVRFLEKRKQELEEACSTLS-H 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 ------LTIKKDAVKDRTLIEQKTLSIHSKLTDKSWQ-LEKEIDSFSAFSNTASAE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 SIATLQESTTLLKDSTTNLHAVESRLIGVMYQDGAESSTVEEASQDDSAQPQDENQSD 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                       7.1%; Score 122.5; DB 2; Length 580; 22.7%; Pred. No. 0.0074; tive 51; Mismatches 98; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ...
STATE: New York
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: LIVDAL, Shunel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30,946
                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 22.74
Matches 54; Conservative
                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-079-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-104-324B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

7;

Search completed: August 13, 2002, 09:24:18 Job time: 149 sec

Sequence:

е О

Run

Searched:

```
Ogama4 chiamydia t
Ogambo chiamydia t
Ogama5 chiamydia t
Ogama5 chiamydia t
Og6711 chiamydia t
Ogycp2 aeropyrum p
Ogycp2 aeropyrum p
Ogycp3 earobycum p
Og532j6 arabidopsis
O15738 dictyosteli
O54874 rattus norv
                                                                                                                                                                                                                                      044929 drosophila 094926 drosophila 09421 homo sapien 04534 loligo peal 0454934 loligo peal 09522 thermotoga 09525 thermotoga 09525 thermotoga 09525 thermotoga 09525 mono sapien 09525 mono sap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O04010 onchocerca
O88938 mus musculu
Q00720 group g str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 oryza sativ
onchocerca
               chlamydia t
chlamydia t
chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parallum-crt.,

MEDLINE-95302975; PubMed-7783634;

Rockey D.D., Heinzen R.A., Hackstadt T.;

"Cloning and characterization of a Chlamydia psittaci gene coding for a protein localized in the inclusion membrane of infected cells.";

Mol. Microbiol. 15:617-626(1995).

EMBL; L35036; AAC41443.1;

SEQUENCE 355 AA; 38802 MW; 335AAD114D226351 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTVSTDNTSPVISRASSPIFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 1733; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.3e-93;
Matches 355; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE LOCALISED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                      Q962Q0
Q9F7L1
Q9YCP2
                                                                                                                                 Q96JV2
Q93ZJ6
                                                                                                                                                                                                                                                                                                                                                             Q9KK49
Q9X252
Q9AS76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       088528
094DC2
004010
088938
000720
                                                                                                                                                                                                 054874
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9KKP6
                                                                                                                                                                                                                                                                                                                       Q15075
O44934
                                                                                                                                                                                                                                                                                                    014221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         046210 PRELIMINARY;
046210;
01-NOV-1996 (TEMBLE-1 01, Cr
01-NOV-1996 (TEMBLE-1 01, La
01-DEC-2001 (TEMBLE-1 19, La
          4 4 4 7 7 7 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 0 
      Chlamydophila caviae.
      SEQUENCE FROM N.A.
                                                                 150.5
157.5
157.5
150.5
149
149
146.5
145.5
145.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.5
143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-GPIC
  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                  August 13, 2002, 09:24:04 ; Search time 48.57 Seconds (without alignments) 1264.427 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q46210 chlamydophi
Q53263 chlamydia p
Q9288 chlamydia p
Q92688 chlamydia t
Q9m94 chlamydia t
Q9am94 chlamydia t
Q9am94 chlamydia t
Q94121 chlamydia t
Q99789 chlamydia t
Q9778 chlamydia t
Q9778 chlamydia t
Q9778 chlamydia t
Q95196 chlamydia t
Q9am2 chlamydia t
Q9am2 chlamydia t
Q9am2 chlamydia t
Q9am8 chlamydia t
Q9am8 chlamydia t
Q9am8 chlamydia t
Q9am8 chlamydia t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                         1733
1 MIVSTDNISPVISRASSPIF......DDSAQPQDENQSDAGEHKDS 355
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q46210
Q53263
Q92828
Q9PKR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AM94
O84121
Q99Q56
Q9F7K9
O69196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09AMB2
09AMA8
09AMA6
09AMB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_lnvertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AMA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AMA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                              Inimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                            US-09-673-763-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
273
273
273
273
273
273
273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448
200
166.5
164.5
164.5
164.5
163.5
162.5
162.5
161.5
161.5
                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
```

٠ و

Result

ö

9

```
STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PKR8
Q9PKR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q9PKR8
ID Q99
AC Q99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
     δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGAE---SSTVEEAS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 SEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVETMLSPFEKLA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92333842; PubMed=1821438; MEDLINE-92333842; PubMed=1821438; Sato C., Katumata A., Takashima I., Hashimoto N.; Sato C., Katumata A., Takashima I., Hashimoto N.; Nucleotide sequence of a gene encoding a new genus specific protein of Chlamydia psittaci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 OSLKETFSQEAVQAMMSSVTELRTNLNALKELITENKTVIEQLKADAQLREEQVRFLEKR
                                   241 TNLNALKELITENKTVIEQLKADAQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTT
                                                                                                                                                                                                                                                              LLKDSTTNLHAVESRLIGVMVQDGAESSTVEEASQDDSAQPQDENQSDAGEHKDS 355
                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.9%; Score 448; DB 2; Length 22:
ilarity 46.9%; Pred. No. 7.1e-19;
Conservative 44; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA; 25165 MW; 74C3D808E749A8FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILARITY TO CT119 INCA (CPJ0186 PROTEIN).
CPN0186 OR CP0181.
CPN0186 OR CP0181.
CALIAMYDIA pneumoniae (Chlamydophila pneumoniae).
CALIAMYDIA CALIAMYDIA CHAMYDIA CHAMYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 25.2 KDA PROTEIN (FRAGMENT).
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jpn. J. vet. Res. 39:159-165(1991).
EMBL, S40167; AAB22558.2;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCDLRDPSGDRYGGWG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDDSAQPQDENQSDAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         092828
092828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 053263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                053263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                 181
                                                                                                                                                                                                                                                                                   301
                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
092828
1D 082828
1D 099
AC 099
DT 001
DT 000
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q53263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                             Dp
                                                                                                        Ω
                                                                                                                                                                       Qγ
                                                              δ
```

```
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 LREEQVRFLEKRKQELEEACSTLSHSIATLQESTTLLKDSTTNLHAVESRLIGVMVQDGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGGEBRRLREEVSRFTSENQRLTVITTLETEVKDLKAAKDQLTLEIEAFRNENGNLKTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 FEKLAQSLKETFSQBAVQAMMSSVTELRTNLNALKELI------TENKTVIEQLKADAQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTRVVGELLESENKLSQACSALRQEIEKLAQHETSLQQRIDAMLAQEQNL-----A 317
                                                                                                                                                                                                                                                                                                                                                     STRAIN-AR39;
MEDLINE=2015055; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-203030349; PubMed-10871362;
MEDLINE-203030349; PubMed-10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Rishi F., Ouchi K.,
Shiba T., Ishli K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).

Nucleic Acids Res. 28:2311-2314(2000).

EMBL; AE001605; AAD18339.1;
EMBL; AE002217; AAF88399.1;
EMBL; AP002545; BAA98396.1;
THSSP; PO55412; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 -----QALKVLLGGEWVQEAQTHVKAMQEQIQALQAEILGMHNOSTALQKSVENLLVQDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TSPVISRASSPTFGDHGKDFDNNKIIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPVNNTPSAPN-----KPRSSFIEKVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKIIAAIALFVVGIAALVCLYLGSVIS----TPSL-ILMLAIMLVSFVIVITAIRDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 -VELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKS-VGTKVETMLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| || :: | | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | : | | :: | | : | | :: | | :: | | : | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 200; DB 16; Length 390; 23.0%; Pred. No. 0.00031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ll protein; Complete proteome.
390 AA; 42507 MW; F78B8469760A4FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 PSQVVRHMKQQIQQFGEEN-----TRLHTAVENLKAVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 EQVTALEKMKQEAQKAESE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 ESSTVEEASQDDSAQPQDE 344
                                                                                                                                                                             Genet. 21:385-389(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 23.0%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
```

2

```
lack IncA, a protein localized to the inclusion membrane."; Infect. Immun. 68:360-367(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-IC-CALB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09AMA9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AMA9
                                     RTI
REPRESENTATION OF THE REPRESENTATION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                  STRAIN-MOPN / NIGG;
MEDLINE-20150255; PubMed-10684935;
MEDLINE-20150255; PubMed-10684935;
Mead T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Elsen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-D(S) 2923;
MEDLINE-20072706; PubMed-10603409;
Suchland R.J., Rockey D.D., Bannantine J.P., Stamm W.E.;
"Isolates of Chlamydia trachomatis that occupy nonfusogenic inclusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 AIALFVVGIAALVCLYLGSVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVRHMKQQI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLEEFKSVGTKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKEL---- 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 QQFGEENTRLHTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 ASLKEVNFL-----LKSVQKEF---LGLSKDFATTSKDLSD----VSLDFHNLLQDFQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 RRLAENKEDLLKIVQDLQDIRDK----LRAEINNLSQASKTLSEQIASQIEENEKLYANI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SSPTFGDHGKDFDNNKIIPISIEAP--TSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||| : :||: | | | | | | | : : : : :||: | : : | | : : : : :||: | : : : :||: | : : : : :||: | : : : :||: | : : : :||: | : : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: | : : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: : :||: :||: : :||: : :||: : :||: : :||: : :||: : :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ITENKTVIEQLKADAQ-LREEQVRFLEKRKQELEEACSTLSHSIAT-LQESTTLLKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 185; DB 16; Length 276;
Pred. No. 0.0015;
4; Mismatches 121; Indels 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 276 Aa; 30744 MW; F3C2D59A2BACD51A CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE LOCALISED PROTEIN INCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                          Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE002306; AAF39253.1;
TIGR; TC0396; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 TINL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 TKAL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09RFX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9RFX7
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Pannekock Y., van der Ende A., Eljk P.P., van Marle J., de Witte M.A., Ossewaarde J.M., Morre S.A., van den Brule A.J.C., Dankert J.;

"Normal Inca expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the inca IA77 mutation.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF126733; AAM11237.1;

EMBL, AF326996; AAG61093.1;

EMBL, AF327327; AAK11231.1;

EMBL, AF327328; AAK11231.1;

EMBL, AF327328; AAK11231.1;

EMBL, AF327328; AAK11231.1;

EMBL, AF327328; AAK11231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UW-4;
MEDLINE-21295121; PubMed-11402010;
MEDLINE-21295121; PubMed-11402010;
Pannekoek Y., van Der Ende A., Elly P.P., van Marle J., de Witte M.A.,
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Normal IncA expression and fusogenicity of inclusions in Chlamydia
trachomatis isolates with the incA 147T mutation.";
Infect. Immun. 69:4654-4656(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 LYLGSVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 --EVGSLKEINFMLS--VLOKKFLH----LSKEFATTSKDLSAVSODFYSCLOGFRDNY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 HTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 TKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK----- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVV----GIAALVC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 -TVIEQLKA-DAQLREE--QVRFLEK------RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 TVVIEBLKTIRDSLRDEIGQLSQLSQLSGTALTSQIALQRKESSDLCSQIRETLSSPRKSAS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
SEQUENCE FROM N.A. STAIN MT9291, AND MT9336; STAIN-MT93946, MT9334, MT9291, AND MT9336; STAIN-MT93940 N. Sockhand R.J.; Stamm W.E.; "Diverse Mutations in incA Amplified from Clinical Chiamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 166.5; DB 2; Length 273; 23.5%; Pred. No. 0.018; vative 57; Mismatches 104; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30314 MW; 9D0C862A533FDE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 AA.
```

11;

SO

```
Local Similarity
nes 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MT9301;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MT459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete | SEQUENCE
                                                                   084121
084121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                          8
  214
                                            RESULT
084121
                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
     op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK------TVI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQ1QQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSLKEINFMLS--VLOKEFLH-----LSKEFATTSKDLSAVSODFYSCLQGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILDEYKNSTEEMRKLFSQEITADLKGSVASLREEIRFLTPLAEEVRRLAHNQOSLTVVI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                     101 GSLKEINFMLS--VLOKEFLH-----LSKEFATTSKDLSAVSQDFYSCLQGFRDNYKGFE 153
                                                                           Gaps
                                                                                                  32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTPPSPPAPSYSANRV-----PQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLIAPQITIVLLALFIISLA------GNALYLQKTANLHLYQDLQR-----EV
                                                                                                                                                        SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV
                                                                                                                                                                                                             ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE
                                                                                                                         8 VTPPSPPAPSYSANRV------POPSLMDKIKKIAAIASLILIGTIGFLALLGHLVG
                                                                                                                                                                                  59 FLITPQITIVLLALFIISLA------GNALYLQKTANLHLYQDLQR-----EV
                                                                                                                                                                                                                                                                                         SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQQSLTVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 EQLKA-DAQLREE--QVRFLEK-----RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                    258 EQLKA-DAQLREE--QVRFLEK-----RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
"Diverse Mutations in incA Amplified from Clinical Chlamydia
trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AS227326; ARX11220.1; --
SEQUENCE 273 AA; 30354 MW; 6945AE6A0D5092C3 CRC64;
                                               Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                           Indels
                                                                                                                                                                                                                                                                  TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK ---
         61FA8F2085701F58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 164.5; DB 2;
22.8%; Pred. No. 0.023;
Live 59; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                Score 164.5; DB 2;
Pred. No. 0.023;
9; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                    273 AA
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                   th 9.5%; Scools 1.5%; Scools 1.5%; Scools 1.5%; Proceed 59; Conservative 59;
003; AAG61100.1; -. 273 AA; 30357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=MT9227;
  AF327003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001
                                                       Query Match
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AM94;
                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                         09AM94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
    EMBL;
                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q9AM94
```

g

g

δ

g ŏ

ŏ

q

Qγ

```
٠
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Witte M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 273;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.; "Diverse Mutations in incA Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.; "Diverse Mutations in incA Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6945AE7E8B8BEBF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 164.5; DB 1b;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID-813;
                                                                                                                                                                                                                                                                                   273
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF327006; AAG61103.1;
AF327012; AAG61109.1;
AF327014; AAG61111.1;
AF327015; AAG61112.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF326998; AAG61095.1;
EMBL; AF327002; AAG61099.1;
EMBL; AF327004; AAG61101.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF326992; AAK11233.1;
AF326992; AAG61089.1;
AF326994; AAG61091.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
```

10;

pp

Ω

δλ g òγ

δλ g

δ QQ

1

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          069196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
         à
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                       | :| :| || :| :| || GSLKEINFMLS--VLQKEFLH-----LSKEFATTSKDLSAVSQDFYSCLGGFRDNYKGFE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEBNTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
                                                                                                                                                                                                                                                                                                                                                                                                                          32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                           TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRINLNALKELITENK------TVI
                                                                                                                                                                                                                                                                                                                                                                                                                                        208 TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK------TVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQLKA-DAQLREE--QVRFLEK------RKQELEEACSTLSHSIATLQESTT 300
                                                                                                               258 EQLK-ADAQLREE--QVRFLEK-----RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MT9329, AND MT9339;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
"Diverse Mutations in inch Amplified from Clinical Chlamydia
"Inverse Mutations in the Amplified from Clinical Chlamydia
trachomatis Isolates that Occupy Nonfusogenic Inclusions.";
EMBL; AF327331; AAX11235.1;
EMBL; AF327330; AAX11234.1;
SEQUENCE 273 AA: 30339 MW; B445B3638BBEBE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      / Match 9.4%; Score 163.5; DB 2; Length 273; Local Similarity 22.8%; Pred. No. 0.027; nes 67; Conservative 59; Mismatches 109; Indels 59
                                                                                                                                                                                        01-JUN-2001 (TIEMBLIEL 17, Created)
01-JUN-2001 (TIEMBLIEL 17, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09F7K9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                   Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 AA.
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                        Chlamydia trachomatis.
                                                                                                                                                                                                                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                      099056
        59
                          148
                                            101
                                                               208
                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9F7K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
09F7K9
                                         g
                         à
                                                          à
                                                                              g
                                                                                                   ò
                                                                                                                    g
                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE DE LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
SECUENCE FROM N.A.

SECUENCE FROM N.A.

SC STRAIN=7A, DK-20, MRC-301, 4A, AND 12A;

A Pannekoek Y., van der Ende A., Eilk P.E., van Marle J., de Witte M.A.,

RA Pannekoek Y., van der Ende A., Eilk P.E., Dankert J.;

RT trachomatis isolates with the inca latt mutation. ";

RT trachomatis isolates with the inca 147r mutation.";

DR EMBL; AF279354, AAG31469.1; -..

DR EMBL; AF327001; AAG61103.1; -..

DR EMBL; AF327001; AAG61098.1; -..

DR EMBL; AF327011; AAG61108.1; -..

DR EMBL; AF37011; AAG61108.1; -..

DR EMBL; AF37011; AAG61108.1; -..

DR EMBL; AF37011; AAG6110.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLIKE-99043938; PubMed-9826388; Bannantine J.P., Stamm W.E., Suchland R.J., Rockey D.D.; Bannantine J.P., Stamm W.E., Suchland R.J., Rockey D.D.; "Chlanydia trachomatis IncA is localized to the inclusion membrane and Is recognized by antisera from infected humans and primates."; Infect. Immun. 66:6017-6021(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 LYLGSVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 HTAVENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 TKVETMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK------ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVV----GIAALVC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 -TVIEQLKA-DAQLREE--QVRFLEK------RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111:11 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 HLVGFLIAPQITIVLLALFIISLA-----GNALYLQKTANLHLYQDLQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                          Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.; "Diverse Mutations in incA Amplified from Clinical Chlamydia trachomatis Isolates that Occupy Nonfusogenic Inclusions."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.4%; Score 162.5; DB 2; Length 23.2%; Pred. No. 0.031; Live 58; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID~813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.29
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCLUSION MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID-813;
                                                                                                                                                                                                                                                             STRAIN-MT5942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LGV-434;
```

SO

```
MEDLINE=21295121; PubMed=11402010; Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A., Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.; Normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA 147T mutation."; Infect. Immun. 69:4654-4656(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRT--------NLNALKELI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 FLIAPQITIVLLALFITSLA-----GNALYLOKTANLHLYQDLQR------EV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TENKTVIEQLKAD----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 | | | : : |: : :| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| : ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
---RKQELEEACSTLSHSIATLQESTT 300
                                     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-UW-12;
MEDLINE-21295121; PubMed-11402010;
Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30318 MW; 22729569405E422B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                 01-JUN-2001 (TIEMBLEEL. 17, Created)
01-JUN-2001 (TIEMBLEEL. 17, Last sequence update)
01-DEC-2001 (TIEMBLEEL. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.3%; Score 161.5; DB Best Local Similarity 21.4%; Pred. No. 0.035; Matches 63; Conservative 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 AA
                                                                                                                                                                                                                                  PRT;
             EQLKA-DAQLREE--QVRFLEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9AMA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9AMA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                                               13
                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMA8
                                                                                                                                                                               RESULT
                                                                                                                                                                                                             Q9AMB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                    g
                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-UW-31;
MEDLINE-21295121; PubMed-11402010;
MEDLINE-21295121; PubMed-11402010;
Pannekoek Y., van Der Ende A., Eijk P.P., van Marle J., de Witte M.A., Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
"Normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA 147T mutation.";
Infect. Immun. 69:4654-4656(2001).
EMBL: AF327007; AAG61104.1; .
SEQUENCE 273 AA; 30337 MW; 6945AE7EBBB824F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 FLIAPQITIVLLALFIISLA-----GNALYLQKTANLHLYQDLQR------EV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK------TVI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NLNALKELI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                            SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV
                                                                                                                                                                                                                                                  32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG
                                                                                                                                                                                                                                                                                           :|: | :|: | :|: | 59 FLIAPQITIVLLALFITSLA------GNALYLQKTANLHLYQDLQR------EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLIDEYKNSTEEMRKLFSQEITADLKGSVASLREEIRFLTPLAEEVRRLAHNQESLTAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 TENKTVIEQLKAD----AQLREEQVRFLEKRKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 273;
                                                                                                                            Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                            Indels
                                 E64B846A5D6824EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.4%; Score 162.5; DB 2; 22.8%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                         ch 9.4%; Score 162.5; DB 2;
1 Similarity 21.4%; Pred. No. 0.031;
63; Conservative 61; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
          EMBL; AF067958; AAC82641.1; -. SEQUENCE 273 AA; 30272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.8
nes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                             y Match
Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9AMA7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9AMA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
09AMA7
10 09AMA7
AC 09AMA7
DT 01-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
                                                                                                                                             Query Mat
Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
```

q Óλ q

g δy g ò 8;

Gaps

28 16

213

de Witte

QQ

a

ò

RE SO SO

g Q q Qγ

δ

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-440-L;
STRAIN-440-L;
MEDLINE-21295121; PubMed-11402010;
Pannekoek Y., van Der Ende A., Eljk P.P., van Marle J., de Witte M.A.,
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
Normal IncA expression and fusogenicity of inclusions in Chlamydia trachomatis isolates with the incA I47T mutation.";
Infect. Immun. 69.4654-4656(2001).
EMBL; AF327008; AG61105.1;
SEQUENCE 273 AA; 30265 MW; 2267957C555E572B CRC64;
                                                                                                                                                                                                                                                                             92 SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                               148 ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYĻVKIIAAIALFVVGIAALVCLXLG 91
Ossewaarde J.M., van Den Brule A.J.C., Morre S.A., Dankert J.;
"Normal IncA expression and fusogenicity of inclusions in Chlamydia
trachomatis isolates with the incA 147T mutation.";
Infect. Immun. 69:4654 4656 (2001).
EMBL; AF327005; AAG61102.1;
SEQUENCE 273 AA: 30387 MW; 6945AE7E9BBAEBER3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 SVISTPSLILMLAIMLVSFVIVITAIRDGTPSQVVR----HMKQQIQQFGEENTRLHTAV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 FLIAPQITIVLLALFITSLA------GNALYLQKTANLHLYQDLQR------EV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ENLKAVNVELSEQINQLKQLHTRLSDFGDRLEANTGDFTALIADFQLSLEEFKSVGTKVE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 IIPISIEAPTSSAAAVGAKTAIEPEGRSPLLQRICYLVKIIAAIALFVVGIAALVCLYLG 91
                                                                                                                                                                                                                                                                                                   :|: |::||::||
59 FLIAPQITIVLLALFIISLA------GNALYLQKTANLHLYQDLQR-----EV
                                                                                                                                                                                                                                                                                                                                                                                                                                               154 SLLDEYKNSTEEMRKLFSQEIIADLKGSVASLREEIRFLTPLAEEVRRLAHNQQSLTVVI
                                                                                                                                                                                                                                                                                                                                                                                                                  208 TMLSPFEKLAQSLKETFSQEAVQAMMSSVTELRTNLNALKELITENK------TVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 VTPPSPPAPSYSANRV------PQPSLMDKIKKIAAIASLILIGTIGFLALLGHLVG
                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 EQLKA-DAQLREE--QVRFLEK-----RKQELEEACSTLSHSIATLQESTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 273;
                                                                                                                                            9.3%; Score 161.5; DB 2; Length; 22.8%; Pred. No. 0.035; tive 58; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INCLUSION MEMBRANE PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.3%; Score 161.5; DB 2;
Best Local Similarity 21.4%; Pred. No. 0.035;
Matches 63; Conservative 61; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                  Query Match
Best Local Similarity 22.8%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09AMA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
09AMA6
AC 09AMA6
AC 09AMA6
DT 01-JUN
DT 01-DEC
DE INCLUS
OS Chlamy
OC Bacter
OX NCBL
TRN (1)
RP SEQUEN
RC STRAIN
RX MEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AMA6
 RT
RT
RL
DR
SQ
                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                       윱
                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                   염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

Search completed: August 13, 2002, 09:30:16 Job time: 372 sec